

NR Native PVIIA Search:

## BLASTP 2.2.4 [Aug-26-2002]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038287392-07658-24371

### Query=

(27 letters)

**Database:** All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

1,242,768 sequences; 395,571,179 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

### Distribution of 156 Blast Hits on the Query Sequence

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Sequences producing significant alignments:	Score (bits)	E Value
<a href="#">gi 7519866 pir  A58997</a> kappa-conotoxin PVIIA - cone shell (...)	98	9e-21
<a href="#">gi 22002036 sp P56633 CXK7</a> CONPU Kappa-conotoxin PVIIA prec...	98	9e-21
<a href="#">gi 3891872 pdb 1KCP </a> 3d Structure Of K-Conotoxin Pviia, A ...	93	4e-19
<a href="#">gi 3891964 pdb 1AV3 </a> Potassium Channel Blocker Kappa Conot...	93	4e-19
<a href="#">gi 1905981 gb AAB50229.1 </a> Gal/GalNAc lectin heavy subunit [...]	33	0.32
<a href="#">gi 17158399 ref NP 477819.1 </a> wsv297 [shrimp white spot synd...	30	2.5
<a href="#">gi 15895618 ref NP 348967.1 </a> Glycosyltransferase [Clostridi...	29	8.1
<a href="#">gi 10120503 pdb 1C6W A</a> Chain A, Maurocalcin From Scorpio Ma...	28	11
<a href="#">gi 19577387 emb CAD27769.1 </a> hypothetical protein [Anopheles...	28	11
<a href="#">gi 21402496 ref NP 658481.1 </a> minC, Bacterial proteins invol...	28	15
<a href="#">gi 23021387 gb ZP 00061064.1 </a> hypothetical protein [Clostri...	28	15
<a href="#">gi 17567271 ref NP 510129.1 </a> Predicted CDS, p-glycoprotein ...	28	15
<a href="#">gi 20454175 gb AAM22197.1 AF501276 1</a> Gal/GalNAc lectin heav...	27	19
<a href="#">gi 7494127 pir  T09229</a> galactose binding adhesin heavy chai...	27	19

gi 22476954 gb AAM97358.1	Gal/GalNAc lectin heavy subunit ...	27	19
gi 2133404 pir  S70663	lectin heavy chain, N-acetylgalactos...	27	19
gi 22964283 gb ZP_00011889.1	hypothetical protein [Rhodops...	27	19
gi 17563788 ref NP_507195.1	Predicted CDS, 7 transmembrane...	27	26
gi 21703938 ref NP_663450.1	ceramide kinase [Mus musculus]...	27	26
gi 543793 sp P36953 AFAM RAT	Afamin precursor (Alpha-albumi...	27	26
gi 23510111 ref NP_702777.1	erythrocyte membrane protein 1...	27	35
gi 17508479 ref NP_493155.1	Nuclear Hormone Receptor famil...	27	35
gi 17569649 ref NP_510122.1	Predicted CDS, zinc finger C4 ...	26	47
gi 23612818 ref NP_704357.1	hypothetical protein [Plasmodi...	26	47
gi 23613070 ref NP_703392.1	hypothetical protein [Plasmodi...	26	63
gi 23123030 gb ZP_00105165.1	hypothetical protein [Prochlo...	26	63
gi 21302332 gb EAA14477.1	agCP8528 [Anopheles gambiae str....	26	63
gi 21288202 gb EAA00523.1	agCP9342 [Anopheles gambiae str....	26	63
gi 17538866 ref NP_501730.1	Zinc finger C4 type Ligand-bin...	25	85
gi 17068427 gb AAH17594.1 AAH17594	Unknown (protein for MGC...	25	85
gi 17567269 ref NP_510128.1	P-glycoprotein family member (...	25	85
gi 20454177 gb AAM22198.1 AF501277_1	Gal/GalNAc lectin heav...	25	85
gi 2133405 pir  S70664	lectin heavy chain, N-acetylgalactos...	25	85
gi 11359716 pir  T46722	conserved hypothetical protein [imp...	25	85
gi 23510154 ref NP_702820.1	RNA-binding protein of pumilio...	25	85
gi 15450391 gb AAK96489.1	At2g16530/F1P15.9 [Arabidopsis t...	25	85
gi 20454179 gb AAM22199.1 AF501278_1	Gal/GalNAc lectin heav...	25	85
gi 6322428 ref NP_012502.1	Protein required for cell viabi...	25	85
gi 14250071 gb AAH08440.1 AAH08440	Similar to CGI-29 protei...	25	85
gi 8953421 emb CAB96572.1	AmphiGli protein [Branchiostoma ...	25	85
gi 399540 sp P32022 GIL1 ENTHI	GALACTOSE-INHIBITABLE LECTIN...	25	85
gi 14290597 gb AAH09077.1 AAH09077	CGI-29 protein [Homo sap...	25	85
gi 7705724 ref NP_057041.1	CGI-29 protein [Homo sapiens] >...	25	85
gi 10638481 emb CAC12642.1	dJ179L10.2 (Similar to CGI-29 p...	25	85
gi 7496642 pir  T19540	hypothetical protein C28D4.1 - Caeno...	25	85
gi 17569651 ref NP_510121.1	Nuclear receptor-like, contain...	25	114
gi 7513590 pir  T42230	AF4 protein - mouse (fragment) >gi 2...	25	114
gi 7661970 ref NP_055455.1	KIAA0173 gene product [Homo sap...	25	114
gi 159019 gb AAA29126.1	alpha-phosphoinositide-specific p...	25	114
gi 17563970 ref NP_506967.1	Zinc finger C4 type family mem...	25	114
gi 125493 sp P07313 KML2 RABIT	Myosin light chain kinase 2, ...	25	114
gi 13359167 dbj BAB33316.1	KIAA1646 protein [Homo sapiens]	25	114
gi 17566198 ref NP_507649.1	Predicted CDS, zinc finger C4 ...	25	114
gi 6572330 emb CAB62977.1	dA59H18.2 (novel protein similar...	25	114
gi 20898146 ref XP_127515.1	similar to hypothetical protei...	25	114
gi 7662550 ref NP_054801.1	PRO0397 protein [Homo sapiens] ...	25	114
gi 25023945 ref XP_204197.1	homolog of human MLLT2 unident...	25	114
gi 125494 sp P20689 KML2 RAT	Myosin light chain kinase 2, s...	25	114
gi 20849986 ref XP_138040.1	similar to ribosomal protein S...	25	114
gi 21553101 ref NP_660128.1	afamin precursor; alpha albumi...	25	114
gi 14993776 ref NP_149109.1	skeletal myosin light chain ki...	25	114
gi 17105364 ref NP_476557.1	myosin light chain kinase 2, s...	25	114
gi 20072386 gb AAH26681.1	Unknown (protein for IMAGE:50644...	25	114
gi 20336726 ref NP_073603.2	ceramide kinase; lipid kinase ...	25	114
gi 13878317 sp O88573 AF4 MOUSE	AF-4 protein (Proto-oncogen...	25	114
gi 393063 gb AAA18296.1	hemagglutinin-neuraminidase >gi 39...	24	153
gi 1621417 gb AAB17181.1	hemagglutinin-neuraminidase [Huma...	24	153
gi 393067 gb AAA03318.1	hemagglutinin-neuraminidase	24	153
gi 1621397 gb AAB17171.1	hemagglutinin-neuraminidase [Huma...	24	153
gi 393053 gb AAA18291.1	hemagglutinin-neuraminidase	24	153
gi 17544200 ref NP_502862.1	Putative secreted or extracell...	24	153
gi 25155182 ref NP_741645.1	Nuclear Hormone Receptor famil...	24	153
gi 1621421 gb AAB17183.1	hemagglutinin-neuraminidase [Huma...	24	153
gi 393047 gb AAA18288.1	hemagglutinin-neuraminidase	24	153
gi 13878219 ref NP_113566.1	ribonuclease/angiogenin inhibi...	24	153

<a href="#">gi 393059 gb AAA18294.1 </a>	hemagglutinin-neuraminidase	<u>24</u>	153
<a href="#">gi 1621409 gb AAB17177.1 </a>	hemagglutinin-neuraminidase [Huma...	<u>24</u>	153
<a href="#">gi 1621413 gb AAB17179.1 </a>	hemagglutinin-neuraminidase [Huma...	<u>24</u>	153
<a href="#">gi 1621405 gb AAB17175.1 </a>	hemagglutinin-neuraminidase [Huma...	<u>24</u>	153
<a href="#">gi 1621419 gb AAB17182.1 </a>	hemagglutinin-neuraminidase [Huma...	<u>24</u>	153
<a href="#">gi 729836 sp P41323 IL6 CANFA</a>	Interleukin-6 precursor (IL-6...	<u>24</u>	153
<a href="#">gi 9629903 ref NP_045936.1 </a>	ORF-C [Walleye dermal sarcoma v...	<u>24</u>	153
<a href="#">gi 393051 gb AAA18290.1 </a>	hemagglutinin-neuraminidase	<u>24</u>	153
<a href="#">gi 13027596 ref NP_076421.1 </a>	hypothetical protein MGC2487 [...	<u>24</u>	153
<a href="#">gi 15231494 ref NP_189706.1 </a>	hypothetical protein; protein ...	<u>24</u>	153
<a href="#">gi 19263653 gb AAH25255.1 </a>	Similar to hypothetical protein ...	<u>24</u>	153
<a href="#">gi 22507470 gb AAH19431.1 </a>	Similar to hypothetical protein ...	<u>24</u>	153
<a href="#">gi 12383068 ref NP_073738.1 </a>	hypothetical protein FLJ21347 ...	<u>24</u>	153
<a href="#">gi 9247084 gb AAF86275.1 </a>	interleukin-6 [Canis familiaris]	<u>24</u>	153
<a href="#">gi 19921116 ref NP_609448.1 </a>	CG12299-PA [Drosophila melanog...	<u>24</u>	153
<a href="#">gi 393049 gb AAA18289.1 </a>	hemagglutinin-neuraminidase	<u>24</u>	153
<a href="#">gi 1621415 gb AAB17180.1 </a>	hemagglutinin-neuraminidase [Huma...	<u>24</u>	153
<a href="#">gi 1621399 gb AAB17172.1 </a>	hemagglutinin-neuraminidase [Huma...	<u>24</u>	153
<a href="#">gi 393069 gb AAA03319.1 </a>	hemagglutinin-neuraminidase	<u>24</u>	153
<a href="#">gi 1621411 gb AAB17178.1 </a>	hemagglutinin-neuraminidase [Huma...	<u>24</u>	153
<a href="#">gi 16588867 gb AAL26923.1 </a>	AF328929_1 interleukin-6 [Canis f...	<u>24</u>	153
<a href="#">gi 10198059 gb AAG15164.1 </a>	nuclear receptor NHR-63 [Caenorh...	<u>24</u>	153
<a href="#">gi 23507986 ref NP_700656.1 </a>	hypothetical protein [Plasmodi...	<u>24</u>	153
<a href="#">gi 1621403 gb AAB17174.1 </a>	hemagglutinin-neuraminidase [Huma...	<u>24</u>	153
<a href="#">gi 1621407 gb AAB17176.1 </a>	hemagglutinin-neuraminidase [Huma...	<u>24</u>	153

## Alignments

Get selected sequences

Select all

Deselect all

>[gi|7519866|pir||A58997](#) kappa-conotoxin PVIIA - cone shell (Conus purpurascens)  
Length = 27

Score = 98.2 bits (224), Expect = 9e-21  
Identities = 27/27 (100%), Positives = 27/27 (100%)

Query: 1 CRIPNQKCFQHLDDCCSRKCNRFNKCV 27  
CRIPNQKCFQHLDDCCSRKCNRFNKCV  
Sbjct: 1 CRIPNQKCFQHLDDCCSRKCNRFNKCV 27

>[gi|22002036|sp|P56633|CXK7 CONPU](#) Kappa-conotoxin PVIIA precursor (Fin-popping peptide)  
Length = 72

Score = 98.2 bits (224), Expect = 9e-21  
Identities = 27/27 (100%), Positives = 27/27 (100%)

Query: 1 CRIPNQKCFQHLDDCCSRKCNRFNKCV 27  
CRIPNQKCFQHLDDCCSRKCNRFNKCV  
Sbjct: 46 CRIPNQKCFQHLDDCCSRKCNRFNKCV 72

>[gi|3891872|pdb|1KCP|](#) 3d Structure Of K-Conotoxin Pviia, A Novel Potassium  
Channel-Blocking Toxin From Cone Snails, Nmr, 22

Structures  
Length = 28

Score = 92.7 bits (211), Expect = 4e-19  
Identities = 26/27 (96%), Positives = 26/27 (96%)

Query: 1 CRIPNQKCFQHLDDCCSRKCNRFNKC 27  
CRI NQKCFQHLDDCCSRKCNRFNKC  
Sbjct: 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 27

>gi|3891964|pdb|1AV3| Potassium Channel Blocker Kappa Conotoxin Pviia From C.  
Purpurascens, Nmr, 20 Structures  
Length = 27

Score = 92.7 bits (211), Expect = 4e-19  
Identities = 26/27 (96%), Positives = 26/27 (96%)

Query: 1 CRIPNQKCFQHLDDCCSRKCNRFNKC 27  
CRI NQKCFQHLDDCCSRKCNRFNKC  
Sbjct: 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 27

>gi|1905981|gb|AAB50229.1| Gal/GalNAc lectin heavy subunit [Entamoeba dispar]  
Length = 1125

Score = 33.3 bits (71), Expect = 0.32  
Identities = 12/17 (70%), Positives = 12/17 (70%), Gaps = 3/17 (17%)

Query: 13 DDCCSRK--CNRFN-KC 26  
DDCCSRK C FN KC  
Sbjct: 700 DDCCSRKSQCGNFNGKC 716

>gi|17158399|ref|NP\_477819.1| wsv297 [shrimp white spot syndrome virus]  
gi|17016693|gb|AAL33299.1| wsv297 [shrimp white spot syndrome virus]  
gi|19481945|gb|AAL89221.1| WSSV353 [shrimp white spot syndrome virus]  
Length = 69

Score = 30.3 bits (64), Expect = 2.5  
Identities = 9/14 (64%), Positives = 10/14 (71%), Gaps = 3/14 (21%)

Query: 12 LDDCCSRKCNRFNK 25  
LD+CC CNRF K  
Sbjct: 29 LDECC---CNRFQK 39

>gi|15895618|ref|NP\_348967.1| Glycosyltransferase [Clostridium acetobutylicum]  
gi|15025361|gb|AAK80307.1|AE007735.10 Glycosyltransferase [Clostridium acetobutylicum]  
Length = 252

Score = 28.6 bits (60), Expect = 8.1  
Identities = 11/24 (45%), Positives = 13/24 (54%), Gaps = 11/24 (45%)

Query: 8 CFQHLDDCCSRK-----CNRFN 24  
CF ++DCC K CNRFN  
Sbjct: 193 CF--IEDCC--KQGIKIYSCNRFN 212

>[gi|10120503|pdb|1C6W|A](#) Chain A, Maurocalcin From Scorpio Maurus  
Length = 33

Score = 28.2 bits (59), Expect = 11  
Identities = 10/21 (47%), Positives = 11/21 (52%), Gaps = 6/21 (28%)

Query: 8 CFQHLD-----DCCSRKCNR 22  
C HL DCCS+KC R  
Sbjct: 3 CLPHLKLCKENKDCCSKKCKR 23

>[gi|19577387|emb|CAD27769.1|](#) hypothetical protein [Anopheles gambiae]  
Length = 257

Score = 28.2 bits (59), Expect = 11  
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 15 CCSRKCNR 22  
CCSRKC+R  
Sbjct: 41 CCSRKCSR 48

>[gi|21402496|ref|NP\\_658481.1|](#) minC, Bacterial proteins involved in chromosomal  
partitioning  
[Bacillus anthracis A2012]  
Length = 228

Score = 27.8 bits (58), Expect = 15  
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 11 HLDDCCS 17  
HLDDCCS  
Sbjct: 21 HLDDCCS 27

>[gi|23021387|gb|ZP\\_00061064.1|](#) hypothetical protein [Clostridium thermocellum ATCC  
27405]  
Length = 143

Score = 27.8 bits (58), Expect = 15  
Identities = 9/18 (50%), Positives = 11/18 (61%), Gaps = 4/18 (22%)

Query: 14 DC---CSRKCNRFNKC V 27  
DC S KC+RF+ CV  
Sbjct: 91 DCVVEDSSPKCDRFDNCV 108

>[gi|17567271|ref|NP\\_510129.1|](#) Predicted CDS, p-glycoprotein family member  
[Caenorhabditis  
elegans]

[gi|7499666|pir|T21269](#) hypothetical protein F22E10.4 - Caenorhabditis elegans  
[gi|3876294|emb|CAA91802.1|](#) C. elegans pgp-15 protein (corresponding sequence F22E10.4)  
[Caenorhabditis elegans]  
Length = 1270

Score = 27.8 bits (58), Expect = 15  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 8 CFQHLDDCCSR 18  
 CFQH CCSR  
 Sbjct: 165 CFQH---CCSR 172

>gi|20454175|gb|AAM22197.1|AF501276.1 Gal/GalNAc lectin heavy subunit region D  
 [Entamoeba histolytica]  
 Length = 372

Score = 27.4 bits (57), Expect = 19  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 92 DDCNSRKSQCGNFNGKCV 109

>gi|7494127|pir||T09229 galactose binding adhesin heavy chain - Entamoeba histolytica  
gi|290649|gb|AAA18828.1| galactose-specific adhesin 170kD subunit  
 Length = 1292

Score = 27.4 bits (57), Expect = 19  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 730 DDCNSRKSQCGNFNGKCV 747

>gi|22476954|gb|AAM97358.1| Gal/GalNAc lectin heavy subunit region D [Entamoeba  
 histolytica]  
 Length = 372

Score = 27.4 bits (57), Expect = 19  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 92 DDCNSRKSQCGNFNGKCV 109

>gi|2133404|pir||S70663 lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba  
 histolytica (fragment)  
gi|993053|gb|AAA75551.1| GalNAc lectin heavy subunit  
 Length = 194

Score = 27.4 bits (57), Expect = 19  
 Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KCV  
 Sbjct: 131 DDCNSRKSQCGNFNGKCV 148

>gi|22964283|gb|ZP\_00011889.1| hypothetical protein [Rhodopseudomonas palustris]  
Length = 559

Score = 27.4 bits (57), Expect = 19  
Identities = 9/12 (75%), Positives = 10/12 (83%), Gaps = 1/12 (8%)

Query: 8 CFQHLDDCCSRK 19  
C+QHLDD SRK  
Sbjct: 49 CYQHLDD-ISRK 59

>gi|17563788|ref|NP\_507195.1| Predicted CDS, 7 transmembrane chemoreceptor family member family

member [Caenorhabditis elegans]

gi|7506996|pir||T24389 hypothetical protein T03E6.2 - Caenorhabditis elegans  
gi|3879369|emb|CAB07277.1| Hypothetical protein T03E6.2 [Caenorhabditis elegans]  
Length = 213

Score = 26.9 bits (56), Expect = 26  
Identities = 8/13 (61%), Positives = 9/13 (69%), Gaps = 3/13 (23%)

Query: 1 CR---IPNQKCFQ 10  
CR + NQKCFQ  
Sbjct: 55 CRTMLVSNQKCFQ 67

Score = 20.2 bits (40), Expect = 2886  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 5 NQKCFQ 10  
N+KCFQ  
Sbjct: 125 NRKCFQ 130

>gi|21703938|ref|NP\_663450.1| ceramide kinase [Mus musculus]  
gi|21624342|dbj|BAC01155.1| ceramide kinases [Mus musculus]  
Length = 531

Score = 26.9 bits (56), Expect = 26  
Identities = 11/21 (52%), Positives = 12/21 (57%), Gaps = 5/21 (23%)

Query: 9 FQHLDDCCS-----RKCNRFN 24  
F HL D S RKC+RFN  
Sbjct: 410 FAHLGDGSSDLILIRKCSRFN 430

>gi|543793|sp|P36953|AFAM RAT Afamin precursor (Alpha-albumin) (Alpha-Alb)  
gi|1363266|pir||A53195 afamin precursor - rat  
gi|456359|emb|CAA53994.1| unnamed protein product [Rattus norvegicus]  
Length = 608

Score = 26.9 bits (56), Expect = 26  
Identities = 10/22 (45%), Positives = 12/22 (54%), Gaps = 9/22 (40%)

Query: 12 LDDCCSRK----CNR-----FN 24  
 L+DCC+RK C R FN  
 Sbjct: 381 LEDCCNRKNPLSCYRHAEDKFN 402

Score = 18.5 bits (36), Expect = 9354  
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
 CF+HL  
 Sbjct: 509 CFEHL 513

>[gi|23510111|ref|NP\\_702777.1|](#) erythrocyte membrane protein 1 (PfEMP1) [Plasmodium falciparum 3D7]  
[gi|6562758|emb|CAB62897.1|](#) erythrocyte membrane protein 1 (PfEMP1) [Plasmodium falciparum 3D7]  
 Length = 2209

Score = 26.5 bits (55), Expect = 35  
 Identities = 12/24 (50%), Positives = 15/24 (62%), Gaps = 8/24 (33%)

Query: 9 FQHLDDC--CSR---KC-NRFNKC 26  
 FQH +DC CS+ KC N +KC  
 Sbjct: 1356 FQHTEDCKSCSKFRIKCDN--DKC 1377

>[gi|17508479|ref|NP\\_493155.1|](#) Nuclear Hormone Receptor family NHR-89 (nhr-89) [Caenorhabditis elegans]  
[gi|7498355|pir||T20208](#) hypothetical protein E03H4.13 - Caenorhabditis elegans  
[gi|3875219|emb|CAB05470.1|](#) C. elegans nhr-89 protein (corresponding sequence E03H4.13) [Caenorhabditis elegans]  
[gi|3875498|emb|CAB04035.1|](#) C. elegans nhr-89 protein (corresponding sequence E03H4.13) [Caenorhabditis elegans]  
 Length = 310

Score = 26.5 bits (55), Expect = 35  
 Identities = 11/20 (55%), Positives = 12/20 (60%), Gaps = 7/20 (35%)

Query: 12 LDD----CCSRKCNRFNKC 27  
 LDD C R C R+NKC  
 Sbjct: 52 LDDQKQFC--RSC-RYNKC 68

>[gi|17569649|ref|NP\\_510122.1|](#) Predicted CDS, zinc finger C4 type Ligand-binding domain of nuclear hormone receptor like family member [Caenorhabditis elegans]  
[gi|7507363|pir||T24650](#) hypothetical protein T07C5.2 - Caenorhabditis elegans  
[gi|3879537|emb|CAA90299.1|](#) Hypothetical protein T07C5.2 [Caenorhabditis elegans]  
 Length = 334

Score = 26.1 bits (54), Expect = 47  
 Identities = 12/26 (46%), Positives = 13/26 (50%), Gaps = 12/26 (46%)

Query: 2 RIPNQKCFQHLDDCCSRKCNRFNKC 27



R+P KC R C RFNKCV  
 Sbjct: 59 RLP--KC-----RHC-RFNKCV 72

>gi|23612818|ref|NP\_704357.1| hypothetical protein [Plasmodium falciparum 3D7]  
gi|23499096|emb|CAD51176.1| hypothetical protein [Plasmodium falciparum 3D7]  
 Length = 1408

Score = 26.1 bits (54), Expect = 47  
 Identities = 11/20 (55%), Positives = 12/20 (60%), Gaps = 8/20 (40%)

Query: 6 QKCFQHLDDCCSRKCNRFNK 25  
 +KCF D SRKCN NK  
 Sbjct: 1008 EKCF---D---SRKCN--NK 1019

>gi|23613070|ref|NP\_703392.1| hypothetical protein [Plasmodium falciparum 3D7]  
gi|23504532|emb|CAD51412.1| hypothetical protein [Plasmodium falciparum 3D7]  
 Length = 2349

Score = 25.7 bits (53), Expect = 63  
 Identities = 9/14 (64%), Positives = 11/14 (78%), Gaps = 1/14 (7%)

Query: 12 LDDCCSRKCN-RFN 24  
 LDD C+ KCN +FN  
 Sbjct: 1975 LDDICNNKCNDKFN 1988

Score = 17.6 bits (34), Expect = 16841  
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 19 KCNRFN 24  
 K NRFN  
 Sbjct: 359 KINRFN 364

>gi|23123030|gb|ZP\_00105165.1| hypothetical protein [Prochlorococcus marinus subsp.  
 pastoris str.  
 CCMP1378]  
 Length = 284

Score = 25.7 bits (53), Expect = 63  
 Identities = 7/10 (70%), Positives = 9/10 (90%)

Query: 10 QHLDDCCSRK 19  
 +HL +CCSRK  
 Sbjct: 211 EHLINCCSRK 220

>gi|21302332|gb|EAA14477.1| agCP8528 [Anopheles gambiae str. PEST]  
 Length = 851

Score = 25.7 bits (53), Expect = 63  
 Identities = 8/15 (53%), Positives = 10/15 (66%), Gaps = 3/15 (20%)

Query: 16 CSRKCN---RFNKCV 27

C RKC+ RF +CV  
 Sbjct: 49 CRRKCDRACRFGRCV 63

>gi|21288202|gb|EAA00523.1| agCP9342 [Anopheles gambiae str. PEST]  
 Length = 382

Score = 25.7 bits (53), Expect = 63  
 Identities = 12/32 (37%), Positives = 17/32 (53%), Gaps = 12/32 (37%)

Query: 1 CRIPN--QKC----FQHLDDCCSRKCNRFNKC 26  
 C +P+ +KC F H DDC ++F KC  
 Sbjct: 160 CPVPDTCEKCDPTFFPH-DDC-----DKFYKC 185

>gi|17538866|ref|NP\_501730.1| Zinc finger C4 type Ligand-binding domain of nuclear hormone  
 receptor like family member [Caenorhabditis elegans]  
gi|15718178|emb|CAC70072.1| Hypothetical protein C28D4.9 [Caenorhabditis elegans]  
 Length = 420

Score = 25.2 bits (52), Expect = 85  
 Identities = 11/24 (45%), Positives = 12/24 (50%), Gaps = 11/24 (45%)

Query: 13 DDC-----CSRKCNRFNKC 27  
 +DC C R C RFNKC  
 Sbjct: 54 EDCEVLQQFRNRC-RAC-RFNKC 75

>gi|17068427|gb|AAH17594.1|AAH17594 Unknown (protein for MGC:714) [Homo sapiens]  
 Length = 242

Score = 25.2 bits (52), Expect = 85  
 Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
 DCCSR+C  
 Sbjct: 10 DCCSRRC 16

>gi|17567269|ref|NP\_510128.1| P-glycoprotein family member (146.9 kD) [Caenorhabditis elegans]  
gi|7499665|pir||T21268 hypothetical protein F22E10.3 - Caenorhabditis elegans  
gi|3876293|emb|CAA91801.1| C. elegans pgp-14 protein (corresponding sequence F22E10.3)  
 [Caenorhabditis elegans]  
 Length = 1327

Score = 25.2 bits (52), Expect = 85  
 Identities = 7/11 (63%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 8 CFQHLDDCCSR 18  
 CFQH CC+R  
 Sbjct: 171 CFQH---CCTR 178

>gi|20454177|gb|AAM22198.1|AF501277.1 Gal/GalNAc lectin heavy subunit region D  
[Entamoeba histolytica]  
Length = 372

Score = 25.2 bits (52), Expect = 85  
Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
DDC SRK C FN KC+  
Sbjct: 92 DDCNSRKSQCGNFNGKCI 109

>gi|2133405|pir||S70664 lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba  
histolytica (fragment)  
gi|993055|gb|AAA75552.1| GalNAc lectin heavy subunit  
Length = 194

Score = 25.2 bits (52), Expect = 85  
Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
DDC SRK C FN KC+  
Sbjct: 131 DDCNSRKSQCGNFNGKCI 148

>gi|11359716|pir||T46722 conserved hypothetical protein [imported] - Leishmania major  
gi|6066445|emb|CAB58387.1| possible proline synthetase associated protein [Leishmania  
major]  
Length = 389

Score = 25.2 bits (52), Expect = 85  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
DCCSR+C  
Sbjct: 89 DCCSRRC 95

>gi|23510154|ref|NP\_702820.1| RNA-binding protein of pumilio/mpt5 family, putative  
[Plasmodium  
falciparum 3D7]  
gi|23498236|emb|CAD49207.1| RNA-binding protein of pumilio/mpt5 family, putative  
[Plasmodium  
falciparum 3D7]  
gi|24849851|gb|AAM44411.1| RNA-binding protein Puf2 [Plasmodium falciparum]  
Length = 514

Score = 25.2 bits (52), Expect = 85  
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 6 QKCFQHLDD 14  
QKCF+H DD  
Sbjct: 392 QKCFEHSDD 400

>gi|15450391|gb|AAK96489.1| At2g16530/F1P15.9 [Arabidopsis thaliana]  
Length = 343

Score = 25.2 bits (52), Expect = 85  
 Identities = 8/10 (80%), Positives = 8/10 (80%), Gaps = 1/10 (10%)

Query: 3 IPNQKCFQHL 12  
 IP QKCF HL  
 Sbjct: 61 IP-QKCF AHL 69

>gi|20454179|gb|AAM22199.1|AF501278.1 Gal/GalNAc lectin heavy subunit region D  
 [Entamoeba histolytica]  
 Length = 372

Score = 25.2 bits (52), Expect = 85  
 Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
 DDC SRK C FN KC+  
 Sbjct: 92 DDCNSRKSQCGNFNGKCI 109

>gi|6322428|ref|NP\_012502.1| Protein required for cell viability; Yjl032wp  
 [Saccharomyces cerevisiae]  
gi|1352969|sp|P47059|YJD2 YEAST HYPOTHETICAL 12.4 KD PROTEIN IN DBP4-BET4 INTERGENIC  
 REGION  
gi|1077805|pir||S56804 hypothetical protein YJL032w - yeast (Saccharomyces cerevisiae)  
gi|1008152|emb|CAA89322.1| ORF YJL032w [Saccharomyces cerevisiae]  
 Length = 104

Score = 25.2 bits (52), Expect = 85  
 Identities = 7/12 (58%), Positives = 9/12 (75%), Gaps = 2/12 (16%)

Query: 9 FQHLLDDCCSRKC 20  
 + HL CCSR+C  
 Sbjct: 6 YHHL--CCSRRC 15

>gi|14250071|gb|AAH08440.1|AAH08440 Similar to CGI-29 protein [Homo sapiens]  
 Length = 242

Score = 25.2 bits (52), Expect = 85  
 Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
 DCCSR+C  
 Sbjct: 10 DCCSRRC 16

>gi|8953421|emb|CAB96572.1| Amphigli protein [Branchiostoma floridae]  
 Length = 1112

Score = 25.2 bits (52), Expect = 85  
 Identities = 13/25 (52%), Positives = 13/25 (52%), Gaps = 8/25 (32%)

Query: 6 QKCFQHLLDDC--CS--RKCNRFNKC 26  
 QKC C CS RKCNR KC

Sbjct: 1013 QKC----SKCKRCSKCRKCNRCKKC 1033

>gi|399540|sp|P32022|GIL1\_ENTHI GALACTOSE-INHIBITABLE LECTIN 170 KD SUBUNIT  
Length = 1276

Score = 25.2 bits (52), Expect = 85  
Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27  
DDC SRK C FN KC+  
Sbjct: 714 DDCNSRKSQCGNFNGKCI 731

>gi|14290597|gb|AAH09077.1|AAH09077 CGI-29 protein [Homo sapiens]  
Length = 242

Score = 25.2 bits (52), Expect = 85  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
DCCSR+C  
Sbjct: 10 DCCSRRC 16

>gi|7705724|ref|NP\_057041.1| CGI-29 protein [Homo sapiens]  
gi|4680697|gb|AAD27738.1|AF132963.1 CGI-29 protein [Homo sapiens]  
Length = 242

Score = 25.2 bits (52), Expect = 85  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
DCCSR+C  
Sbjct: 10 DCCSRRC 16

>gi|10638481|emb|CAC12642.1| dJ179L10.2 (Similar to CGI-29 protein) [Homo sapiens]  
Length = 153

Score = 25.2 bits (52), Expect = 85  
Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 14 DCCSRKC 20  
DCCSR+C  
Sbjct: 10 DCCSRRC 16

>gi|7496642|pir||T19540 hypothetical protein C28D4.1 - Caenorhabditis elegans  
Length = 874

Score = 25.2 bits (52), Expect = 85  
Identities = 11/24 (45%), Positives = 12/24 (50%), Gaps = 11/24 (45%)

Query: 13 DDC-----CSRKCNRFNKC 27  
+DC C R C RFNKC

Sbjct: 96 EDCEVLQQFRNRC-RAC-RFNKCV 117

>gi|17569651|ref|NP\_510121.1| Nuclear receptor-like, contains ligand-binding domain but no

obvious zinc finger family member [Caenorhabditis elegans]

gi|7507364|pir||T24648 hypothetical protein T07C5.3 - Caenorhabditis elegans

gi|3879535|emb|CAA90297.1| Hypothetical protein T07C5.3 [Caenorhabditis elegans]

Length = 319

Score = 24.8 bits (51), Expect = 114

Identities = 8/10 (80%), Positives = 8/10 (80%), Gaps = 1/10 (10%)

Query: 18 RKCNRFNKCV 27

R C RFNKCV

Sbjct: 49 RHC-RFNKCV 57

>gi|7513590|pir||T42230 AF4 protein - mouse (fragment)

gi|2582019|gb|AAB82427.1| mAF4 [Mus musculus]

Length = 1211

Score = 24.8 bits (51), Expect = 114

Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 16 CSRKCNR 22

CSRKC+R

Sbjct: 158 CSRKCDR 164

>gi|7661970|ref|NP\_055455.1| KIAA0173 gene product [Homo sapiens]

gi|20455377|sp|Q14679|Y173 HUMAN Hypothetical protein KIAA0173

gi|1136406|dbj|BAA11490.1| similar to pig tubulin-tyrosine ligase. [Homo sapiens]

Length = 1199

Score = 24.8 bits (51), Expect = 114

Identities = 6/7 (85%), Positives = 7/7 (100%)

Query: 12 LDDCCSR 18

L+DCCSR

Sbjct: 519 LEDCCSR 525

>gi|159019|gb|AAA29126.1| alpha-phosphoinositide-specific phospholipase C-like protein precursor [Euplotes crassus]

gi|228393|prf||1803429A phospholipase C-like protein

Length = 141

Score = 24.8 bits (51), Expect = 114

Identities = 10/16 (62%), Positives = 11/16 (68%), Gaps = 5/16 (31%)

Query: 12 LDDCCSR-K--CNRFN 24

LD CSR K C+RFN

Sbjct: 78 LD--CSRYKPVCDRFN 91

>gi|17563970|ref|NP\_506967.1| Zinc finger C4 type family member (47.8 kD)  
 [Caenorhabditis  
     elegans]  
gi|7507276|pir||T24563 hypothetical protein T06C12.6 - Caenorhabditis elegans  
gi|3879608|emb|CAB03298.1| Hypothetical protein T06C12.6 [Caenorhabditis elegans]  
     Length = 414

Score = 24.8 bits (51), Expect = 114  
 Identities = 11/24 (45%), Positives = 12/24 (50%), Gaps = 11/24 (45%)

Query: 13 DDC-----CSRKCNRFNKCVC 27  
           D+C                  C R C RFNKCVC  
 Sbjct: 67 DNCAVSSTDRYQC-RLC-RFNKCVC 88

Get selected sequences  
 Select all  
 Deselect all

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Nov 25, 2002 1:38 AM  
 Number of letters in database: 395,571,179  
 Number of sequences in database: 1,242,768

Lambda	K	H
0.355	0.288	2.12

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30  
 Gap Penalties: Existence: 9, Extension: 1  
 Number of Hits to DB: 21,155,857  
 Number of Sequences: 1242768  
 Number of extensions: 470271  
 Number of successful extensions: 11171  
 Number of sequences better than 20000.0: 10987  
 Number of HSP's better than 20000.0 without gapping: 10987  
 Number of HSP's successfully gapped in prelim test: 0  
 Number of HSP's that attempted gapping in prelim test: 0  
 Number of HSP's gapped (non-prelim): 11165  
 length of query: 27  
 length of database: 395,571,179  
 effective HSP length: 18  
 effective length of query: 9  
 effective length of database: 373,201,355  
 effective search space: 3358812195  
 effective search space used: 3358812195  
 T: 11  
 A: 40  
 X1: 14 ( 7.2 bits)  
 X2: 35 (14.8 bits)  
 X3: 58 (24.6 bits)  
 S1: 34 (19.2 bits)

S2: 34 (17.6 bits)



## Pat Native PVIIA Search

### BLASTP 2.2.4 [Aug-26-2002]

#### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038287801-011156-13490

#### Query=

(27 letters)

**Database:** Protein sequences derived from the Patent division of GenBank

104,350 sequences; 16,453,681 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

#### Taxonomy reports

#### Distribution of 191 Blast Hits on the Query Sequence

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Sequences producing significant alignments:		Score (bits)	E Value
<a href="#">gi 14107109 gb AAE55963.1 </a>	Sequence 5 from patent US 616546...	27	0.76
<a href="#">gi 14118262 gb AAE59501.1 </a>	Sequence 6 from patent US 6187310	27	0.76
<a href="#">gi 14118260 gb AAE59499.1 </a>	Sequence 3 from patent US 6187310	25	3.3
<a href="#">gi 14107107 gb AAE55961.1 </a>	Sequence 2 from patent US 6165469	25	3.3
<a href="#">gi 14107108 gb AAE55962.1 </a>	Sequence 3 from patent US 616546...	25	3.3
<a href="#">gi 20268211 gb AAM17448.1 </a>	Sequence 29 from patent US 6361964	25	4.4
<a href="#">gi 15797474 emb CAC88318.1 </a>	unnamed protein product [Homo s...	25	4.4
<a href="#">gi 21715796 emb CAD38256.1 </a>	unnamed protein product [Homo s...	25	4.4
<a href="#">gi 21886477 emb CAD42152.1 </a>	unnamed protein product [Homo s...	24	6.0
<a href="#">gi 2302756 emb CAA03163.1 </a>	unnamed protein product [Eimeria...	24	8.0
<a href="#">gi 16243883 gb AAE80395.1 </a>	Sequence 8 from patent US 6284253	24	8.0
<a href="#">gi 4530797 emb CAA03824.1 </a>	unnamed protein product [unident...	24	11
<a href="#">gi 3409411 gb AAC30466.1 I89471</a>	Sequence 1 from patent US 5...	24	11
<a href="#">gi 4530805 emb CAA03827.1 </a>	unnamed protein product [unident...	24	11
<a href="#">gi 3999143 gb AAC92575.1 AR021637</a>	Sequence 3 from patent US...	24	11

<a href="#">gi 4530800 emb CAA03825.1 </a>	unnamed protein product [unident...	<a href="#">24</a>	<a href="#">11</a>
<a href="#">gi 3409412 gb AAC30467.1 I89472</a>	Sequence 2 from patent US 5...	<a href="#">24</a>	<a href="#">11</a>
<a href="#">gi 3409416 gb AAC30471.1 I89476</a>	Sequence 12 from patent US ...	<a href="#">24</a>	<a href="#">11</a>
<a href="#">gi 4530803 emb CAA03826.1 </a>	unnamed protein product [unident...	<a href="#">24</a>	<a href="#">11</a>
<a href="#">gi 20221551 gb AAE87124.1 </a>	Sequence 11 from patent US 6326165	<a href="#">23</a>	<a href="#">14</a>
<a href="#">gi 12822272 gb AAE48713.1 </a>	Sequence 6 from patent US 6107088	<a href="#">23</a>	<a href="#">14</a>
<a href="#">gi 20221546 gb AAE87119.1 </a>	Sequence 4 from patent US 6326165	<a href="#">23</a>	<a href="#">14</a>
<a href="#">gi 12822270 gb AAE48711.1 </a>	Sequence 2 from patent US 6107088	<a href="#">23</a>	<a href="#">14</a>
<a href="#">gi 20221547 gb AAE87120.1 </a>	Sequence 5 from patent US 6326165	<a href="#">23</a>	<a href="#">14</a>
<a href="#">gi 16242616 gb AAE79920.1 </a>	Sequence 20 from patent US 6280975	<a href="#">23</a>	<a href="#">19</a>
<a href="#">gi 410755 emb CAA00367.1 </a>	P.195 [Plasmodium falciparum]	<a href="#">23</a>	<a href="#">19</a>
<a href="#">gi 15118603 gb AAE70697.1 </a>	Sequence 100 from patent US 6232061	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 23330539 gb AAN26530.1 </a>	Sequence 2 from patent US 6432408	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 15141755 emb CAC50180.1 </a>	Orf1 [Hepatitis E virus]	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 1254372 gb AAA95626.1 </a>	Sequence 6 from patent US 5482928...	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 20227333 gb AAE89374.1 </a>	Sequence 36 from patent US 63407...	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 3209904 gb AAC20848.1 I81607</a>	Sequence 2 from patent US 5...	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 3991599 gb AAC85026.1 AR002030</a>	Sequence 52 from patent U...	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 15116726 gb AAE70252.1 </a>	Sequence 7 from patent US 622900...	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 14484312 gb AAE63497.1 </a>	Sequence 1 from patent US 620741...	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 1613525 gb AAB16505.1 </a>	Sequence 2 from patent US 5559095...	<a href="#">22</a>	<a href="#">26</a>
<a href="#">gi 1613542 gb AAB16522.1 </a>	Sequence 19 from patent US 555909...	<a href="#">22</a>	<a href="#">35</a>
<a href="#">gi 1613531 gb AAB16511.1 </a>	Sequence 8 from patent US 5559095...	<a href="#">22</a>	<a href="#">35</a>
<a href="#">gi 14092871 gb AAE51612.1 </a>	Sequence 4 from patent US 613003...	<a href="#">22</a>	<a href="#">35</a>
<a href="#">gi 4000083 gb AAC93515.1 AR023217</a>	Sequence 55 from patent U...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 7224006 gb AAE24173.1 </a>	Sequence 2 from patent US 5891857...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 23342653 emb CAD48690.1 </a>	unnamed protein product [Homo s...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 5946864 gb AAE03769.1 </a>	Sequence 20 from patent US 586654...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 4000084 gb AAC93516.1 AR023218</a>	Sequence 56 from patent U...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 3209905 gb AAC20849.1 I81608</a>	Sequence 4 from patent US 5...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 14100343 gb AAE53483.1 </a>	Sequence 4 from patent US 6140485	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 5946896 gb AAE03801.1 </a>	Sequence 62 from patent US 586654...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 15141758 emb CAC50182.1 </a>	Orf1 [Hepatitis E virus]	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 23342657 emb CAD48692.1 </a>	unnamed protein product [Homo s...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 3014969 gb AAC11849.1 I78815</a>	Sequence 2 from patent US 5...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 4000082 gb AAC93514.1 AR023216</a>	Sequence 54 from patent U...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 1610962 gb AAB13941.1 </a>	Sequence 14 from patent US 5527896	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 3210125 gb AAC21069.1 I81828</a>	Sequence 6 from patent US 5...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 23342661 emb CAD48694.1 </a>	unnamed protein product [Homo s...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 10050761 gb AAE27668.1 </a>	Sequence 30 from patent US 5955318	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 3936646 gb AAC80745.1 I92176</a>	Sequence 8 from patent US 5...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 2489823 gb AAB77959.1 I60068</a>	Sequence 2 from patent US 5...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 14035826 emb CAC38509.1 </a>	unnamed protein product [Homo s...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 592200 gb AAA53807.1 </a>	Sequence 4 from Patent WO 8909834	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 3210124 gb AAC21068.1 I81827</a>	Sequence 5 from patent US 5...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 10057493 gb AAE34399.1 </a>	Sequence 14 from patent US 5977305	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 3994047 gb AAC87475.1 AR007841</a>	Sequence 4 from patent US...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 4000081 gb AAC93513.1 AR023215</a>	Sequence 53 from patent U...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 2095522 gb AAB54354.1 </a>	Sequence 23 from patent US 562282...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 912366 gb AAA71820.1 </a>	Sequence 25 from patent US 5429921...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 20268179 gb AAM17416.1 </a>	Sequence 49 from patent US 6361954	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 5946869 gb AAE03774.1 </a>	Sequence 25 from patent US 586654...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 5946861 gb AAE03766.1 </a>	Sequence 7 from patent US 5866542...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 2095523 gb AAB54355.1 </a>	Sequence 24 from patent US 562282...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 2095515 gb AAB54347.1 </a>	Sequence 16 from patent US 562282...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 5946859 gb AAE03764.1 </a>	Sequence 4 from patent US 5866542...	<a href="#">21</a>	<a href="#">47</a>
<a href="#">gi 20246635 gb AAE95293.1 </a>	Sequence 111 from patent US 6350933	<a href="#">21</a>	<a href="#">63</a>
<a href="#">gi 2489301 gb AAB77437.1 I58938</a>	Sequence 23 from patent US ...	<a href="#">21</a>	<a href="#">63</a>
<a href="#">gi 14118421 gb AAE59660.1 </a>	Sequence 90 from patent US 6187548	<a href="#">21</a>	<a href="#">63</a>
<a href="#">gi 2489300 gb AAB77436.1 I58937</a>	Sequence 10 from patent US ...	<a href="#">21</a>	<a href="#">63</a>
<a href="#">gi 5946881 gb AAE03786.1 </a>	Sequence 47 from patent US 586654...	<a href="#">21</a>	<a href="#">63</a>

<u>gi 17912954 gb AAE83208.1 </u>	Sequence 33 from patent US 6303295	<u>21</u>	63
<u>gi 21260774 emb CAD32599.1 </u>	unnamed protein product [Drosop...	<u>21</u>	63
<u>gi 14112251 gb AAE57668.1 </u>	Sequence 40 from patent US 6177075	<u>21</u>	63
<u>gi 11191607 emb CAC16344.1 </u>	unnamed protein product [uniden...	<u>21</u>	63
<u>gi 12807910 gb AAE43130.1 </u>	Sequence 2 from patent US 6074840	<u>21</u>	63
<u>gi 14118419 gb AAE59658.1 </u>	Sequence 86 from patent US 6187548	<u>21</u>	63
<u>gi 16236295 gb AAE78102.1 </u>	Sequence 9 from patent US 627098...	<u>21</u>	63
<u>gi 270588 gb AAA02097.1 </u>	Sequence 2 from Patent US 4879374	<u>21</u>	63
<u>gi 14118420 gb AAE59659.1 </u>	Sequence 88 from patent US 6187548	<u>21</u>	63
<u>gi 3992185 gb AAC85612.1 AR004027</u>	Sequence 2 from patent US...	<u>21</u>	63
<u>gi 15124758 gb AAE73219.1 </u>	Sequence 84 from patent US 6239270	<u>21</u>	63
<u>gi 6733930 emb CAB69362.1 </u>	unnamed protein product [unident...	<u>21</u>	63
<u>gi 10184354 emb CAC08900.1 </u>	fusion between Aequorea victori...	<u>21</u>	63
<u>gi 14118418 gb AAE59657.1 </u>	Sequence 84 from patent US 6187548	<u>21</u>	63
<u>gi 21899919 emb CAD42378.1 </u>	unnamed protein product [Homo s...	<u>21</u>	63
<u>gi 1830486 gb AAB44940.1 </u>	Sequence 29 from patent US 558745...	<u>21</u>	84
<u>gi 15121888 gb AAE72568.1 </u>	Sequence 4 from patent US 6236946	<u>21</u>	84
<u>gi 1831302 gb AAB45756.1 </u>	Sequence 3 from patent US 5591821	<u>21</u>	84
<u>gi 1611873 gb AAB14852.1 </u>	Sequence 5 from patent US 5541311...	<u>21</u>	84
<u>gi 592412 gb AAA54019.1 </u>	Sequence 2 from Patent WO 8905355 ...	<u>21</u>	84
<u>gi 10063187 gb AAE38127.1 </u>	Sequence 16 from patent US 5993827	<u>21</u>	84
<u>gi 1831307 gb AAB45761.1 </u>	Sequence 13 from patent US 5591821	<u>21</u>	84
<u>gi 15864475 emb CAC88676.1 </u>	unnamed protein product [Homo s...	<u>21</u>	84
<u>gi 21438922 emb CAD34848.1 </u>	unnamed protein product [Homo s...	<u>21</u>	84

## Alignments

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```
>gi|14107109|gb|AAE55963.1|    Sequence 5 from patent US 6165469
gi|14107110|gb|AAE55964.1|    Sequence 6 from patent US 6165469
gi|14118261|gb|AAE59500.1|    Sequence 5 from patent US 6187310
      Length = 1292
```

Score = 27.4 bits (57), Expect = 0.76

Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27

DDC SRK C FN KCV

Sbjct: 730 DDCNSRKSQCGNFNGKCV 747

```
>gi|14118262|gb|AAE59501.1|    Sequence 6 from patent US 6187310
      Length = 1277
```

Score = 27.4 bits (57), Expect = 0.76

Identities = 12/18 (66%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27

DDC SRK C FN KCV

Sbjct: 715 DDCNSRKSQCGNFNGKCV 732

```
>gi|14118260|gb|AAE59499.1|    Sequence 3 from patent US 6187310
```

Length = 1276

Score = 25.2 bits (52), Expect = 3.3

Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27

DDC SRK C FN KC+

Sbjct: 714 DDCNSRKSQCGNFNGKCI 731

>gi|14107107|gb|AAE55961.1| Sequence 2 from patent US 6165469

Length = 1295

Score = 25.2 bits (52), Expect = 3.3

Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27

DDC SRK C FN KC+

Sbjct: 729 DDCNSRKSQCGNFNGKCI 746

>gi|14107108|gb|AAE55962.1| Sequence 3 from patent US 6165469

gi|14118259|gb|AAE59498.1| Sequence 2 from patent US 6187310

Length = 1291

Score = 25.2 bits (52), Expect = 3.3

Identities = 11/18 (61%), Positives = 12/18 (66%), Gaps = 3/18 (16%)

Query: 13 DDCCSRK--CNRFN-KCV 27

DDC SRK C FN KC+

Sbjct: 729 DDCNSRKSQCGNFNGKCI 746

>gi|20268211|gb|AAM17448.1| Sequence 29 from patent US 6361964

Length = 469

Score = 24.8 bits (51), Expect = 4.4

Identities = 12/28 (42%), Positives = 15/28 (53%), Gaps = 12/28 (42%)

Query: 6 QKCF-Q---HLDDCCSRKC-----NRFN 24

Q+CF Q +LDDC C +RFN

Sbjct: 33 QRCFCQVSGYLDLDC---TCDVETIDRFN 57

>gi|15797474|emb|CAC88318.1| unnamed protein product [Homo sapiens]

Length = 596

Score = 24.8 bits (51), Expect = 4.4

Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 8 CFQHLDDC 15

CFQ LDDC

Sbjct: 253 CFQILDDC 260

>gi|21715796|emb|CAD38256.1| unnamed protein product [Homo sapiens]

Length = 537

Score = 24.8 bits (51), Expect = 4.4

Identities = 10/19 (52%), Positives = 11/19 (57%), Gaps = 5/19 (26%)

Query: 11 HLDDCCS-----RKCNRFN 24  
           HL D S RKC+RFN  
 Sbjct: 412 HLGDGSSDLILIRKCSRFN 430

>gi|21886477|emb|CAD42152.1| unnamed protein product [Homo sapiens]  
 Length = 377

Score = 24.4 bits (50), Expect = 6.0

Identities = 8/11 (72%), Positives = 8/11 (72%)

Query: 12 LDDCCSRKCNR 22  
           LDDC SR C R  
 Sbjct: 207 LDDCASRPCQR 217

Score = 18.9 bits (37), Expect = 272

Identities = 6/10 (60%), Positives = 7/10 (70%), Gaps = 1/10 (10%)

Query: 13 DDCCSRKCNR 22  
           DDC S C+R  
 Sbjct: 27 DDCSSH-CDR 35

>gi|2302756|emb|CAA03163.1| unnamed protein product [Eimeria maxima]  
gi|10067156|gb|AAE40146.1| Sequence 2 from patent US 6001363  
 Length = 109

Score = 24.0 bits (49), Expect = 8.0

Identities = 10/19 (52%), Positives = 10/19 (52%), Gaps = 9/19 (47%)

Query: 7 KCFQHLLDDCCSRK--CNRF 23  
           KC CCS K CNRF  
 Sbjct: 52 KC-----CCS-KFCCNRF 63

Score = 17.6 bits (34), Expect = 658

Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 15 CCSR 18  
           CCSR  
 Sbjct: 68 CCSR 71

Score = 16.3 bits (31), Expect = 1589

Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 15 CCSRKC 20  
           CC KC  
 Sbjct: 33 CCCSKC 38

Score = 16.3 bits (31), Expect = 1589  
Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 15 CCSRKC 20  
CC KC  
Sbjct: 28 CCCSKC 33

>gi|16243883|gb|AAE80395.1| Sequence 8 from patent US 6284253  
Length = 498

Score = 24.0 bits (49), Expect = 8.0  
Identities = 15/34 (44%), Positives = 16/34 (47%), Gaps = 12/34 (35%)

Query: 2 RIPNQ--KCFQ-----HLD-DC-CSRKCNRFNKC 26  
R P Q KCF HL +C RKC NKC  
Sbjct: 403 RRPQSLKCFNCGKPGHLARNCRAPRKC---NKC 433

>gi|4530797|emb|CAA03824.1| unnamed protein product [unidentified]  
gi|4530807|emb|CAA03828.1| unnamed protein product [unidentified]  
Length = 95

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKC 27  
CF+HLD +C KC N + +KCV  
Sbjct: 20 CFRHLDEREEC---KCLLN-YKQEGDKCV 44

>gi|3409411|gb|AAC30466.1|I89471 Sequence 1 from patent US 5720959  
Length = 48

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKC 27  
CF+HLD +C KC N + +KCV  
Sbjct: 18 CFRHLDEREEC---KCLLN-YKQEGDKCV 42

>gi|4530805|emb|CAA03827.1| unnamed protein product [unidentified]  
gi|4530815|emb|CAA03831.1| unnamed protein product [unidentified]  
Length = 108

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKC 27  
CF+HLD +C KC N + +KCV  
Sbjct: 33 CFRHLDEREEC---KCLLN-YKQEGDKCV 57

>gi|3999143|gb|AAC92575.1|AR021637 Sequence 3 from patent US 5789198  
Length = 145

Score = 23.5 bits (48), Expect = 11  
Identities = 10/19 (52%), Positives = 10/19 (52%), Gaps = 5/19 (26%)

Query: 1 CRIPNQKCFQHLDCCSRK 19  
C I Q CF DCCS K  
Sbjct: 3 CHIHIQ-CF----DCCSMK 16

>gi|4530800|emb|CAA03825.1| unnamed protein product [unidentified]  
gi|4530810|emb|CAA03829.1| unnamed protein product [unidentified]  
Length = 116

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCVC 27  
CF+HLD +C KC N + +KCV  
Sbjct: 20 CFRHLDEREEC---KCLLN-YKQEGDKCV 44

>gi|3409412|gb|AAC30467.1|I89472 Sequence 2 from patent US 5720959  
Length = 48

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCVC 27  
CF+HLD +C KC N + +KCV  
Sbjct: 18 CFRHLDEREEC---KCLLN-YKQEGDKCV 42

>gi|3409416|gb|AAC30471.1|I89476 Sequence 12 from patent US 5720959  
Length = 48

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCVC 27  
CF+HLD +C KC N + +KCV  
Sbjct: 18 CFRHLDEREEC---KCLLN-YKQEGDKCV 42

>gi|4530803|emb|CAA03826.1| unnamed protein product [unidentified]  
gi|4530813|emb|CAA03830.1| unnamed protein product [unidentified]  
Length = 127

Score = 23.5 bits (48), Expect = 11  
Identities = 12/29 (41%), Positives = 16/29 (55%), Gaps = 13/29 (44%)

Query: 8 CFQHLD---DCCSRKC--NRF----NKCVC 27  
CF+HLD +C KC N + +KCV  
Sbjct: 52 CFRHLDEREEC---KCLLN-YKQEGDKCV 76

>gi|20221551|gb|AAE87124.1| Sequence 11 from patent US 6326165  
Length = 716

Score = 23.1 bits (47), Expect = 14  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CFQHLDD 14  
CF HLDD  
Sbjct: 439 CFMHLDD 445

>gi|12822272|gb|AAE48713.1| Sequence 6 from patent US 6107088  
Length = 178

Score = 23.1 bits (47), Expect = 14  
Identities = 7/14 (50%), Positives = 8/14 (57%)

Query: 3 IPNQKCFQHLDDCC 16  
IP K F H+ CC  
Sbjct: 160 IPENKYFHHMGKCC 173

>gi|20221546|gb|AAE87119.1| Sequence 4 from patent US 6326165  
Length = 737

Score = 23.1 bits (47), Expect = 14  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CFQHLDD 14  
CF HLDD  
Sbjct: 460 CFMHLDD 466

>gi|12822270|gb|AAE48711.1| Sequence 2 from patent US 6107088  
Length = 317

Score = 23.1 bits (47), Expect = 14  
Identities = 7/14 (50%), Positives = 8/14 (57%)

Query: 3 IPNQKCFQHLDDCC 16  
IP K F H+ CC  
Sbjct: 160 IPENKYFHHMGKCC 173

>gi|20221547|gb|AAE87120.1| Sequence 5 from patent US 6326165  
Length = 716

Score = 23.1 bits (47), Expect = 14  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CFQHLDD 14  
CF HLDD  
Sbjct: 439 CFMHLDD 445



>gi|16242616|gb|AAE79920.1| Sequence 20 from patent US 6280975  
Length = 13

Score = 22.7 bits (46), Expect = 19  
Identities = 5/7 (71%), Positives = 7/7 (100%)

Query: 20 CNRFNKC 26  
C++FNKC  
Sbjct: 2 CDKFNKC 8

>gi|410755|emb|CAA00367.1| P.195 [Plasmodium falciparum]  
Length = 1654

Score = 22.7 bits (46), Expect = 19  
Identities = 8/16 (50%), Positives = 10/16 (62%), Gaps = 6/16 (37%)

Query: 8 CFQHLD---DCCSRKC 20  
CF+HLD +C KC  
Sbjct: 1558 CFRHLDEREEC---KC 1570

Score = 16.8 bits (32), Expect = 1184  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 22 RFNK 25  
RFNK  
Sbjct: 1332 RFNK 1335

>gi|15118603|gb|AAE70697.1| Sequence 100 from patent US 6232061  
Length = 520

Score = 22.3 bits (45), Expect = 26  
Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 2/10 (20%)

Query: 8 CFQH--LDDC 15  
CFQH LD C  
Sbjct: 317 CFQHMLDTC 326

>gi|23330539|gb|AAN26530.1| Sequence 2 from patent US 6432408  
Length = 1708

Score = 22.3 bits (45), Expect = 26  
Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
LDD CCSR  
Sbjct: 330 LDDQAFCCSR 339

>gi|15141755|emb|CAC50180.1| Orf1 [Hepatitis E virus]  
Length = 1698

Score = 22.3 bits (45), Expect = 26  
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
           LDD CCSR  
 Sbjct: 321 LDDQAFCCSR 330

>gi|1254372|gb|AAA95626.1| Sequence 6 from patent US 5482928  
gi|3012065|gb|AAC11513.1|I75924 Sequence 6 from patent US 5689048  
 Length = 25

Score = 22.3 bits (45), Expect = 26  
 Identities = 8/13 (61%), Positives = 9/13 (69%), Gaps = 1/13 (7%)

Query: 14 DCCSRKCNRFNKC 26  
           DCC+ CNR KC  
 Sbjct: 14 DCCTGSCNR-GKC 25

>gi|20227333|gb|AAE89374.1| Sequence 36 from patent US 6340740  
gi|23330622|gb|AAN26602.1| Sequence 31 from patent US 6432628  
 Length = 47

Score = 22.3 bits (45), Expect = 26  
 Identities = 7/16 (43%), Positives = 9/16 (56%), Gaps = 7/16 (43%)

Query: 7 KCFQHL-----DDC 15  
           KCFQ+L +DC  
 Sbjct: 18 KCFQNLGFVTVHNDC 33

>gi|3209904|gb|AAC20848.1|I81607 Sequence 2 from patent US 5710019  
 Length = 513

Score = 22.3 bits (45), Expect = 26  
 Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 11 HLDDCCSR 18  
           HLD CC R  
 Sbjct: 160 HLDGCKR 167

>gi|3991599|gb|AAC85026.1|AR002030 Sequence 52 from patent US 5739281  
 Length = 4544

Score = 22.3 bits (45), Expect = 26  
 Identities = 10/19 (52%), Positives = 13/19 (68%), Gaps = 5/19 (26%)

Query: 11 HLDDCCSRKC--NRFN-KC 26  
           HL CS+KC N+F+ KC  
 Sbjct: 1230 HLK--CSQKCDQNKFSVK 1246

Score = 20.2 bits (40), Expect = 113  
 Identities = 11/26 (42%), Positives = 14/26 (53%), Gaps = 7/26 (26%)

Query: 1 CRIPNQKCFQHLDDCCSRKCNRFNKC 26  
 CR NQ+C L S +CN F+ C  
 Sbjct: 3749 CR--NQRC---L--SSSLRCNMFDDC 3767

Score = 17.2 bits (33), Expect = 883  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 21 NRFN 24  
 NRFN  
 Sbjct: 443 NRFN 446

Score = 14.6 bits (27), Expect = 5150  
 Identities = 3/4 (75%), Positives = 4/4 (100%)

Query: 12 LDDC 15  
 LD+C  
 Sbjct: 2339 LDEC 2342

Score = 13.4 bits (24), Expect = 12442  
 Identities = 4/5 (80%), Positives = 4/5 (80%)

Query: 17 SRKCN 21  
 SR CN  
 Sbjct: 89 SRLCN 93

>gi|15116726|gb|AAE70252.1| Sequence 7 from patent US 6229005  
gi|21508670|gb|AAM58155.1| Sequence 7 from patent US 6379891  
 Length = 1693

Score = 22.3 bits (45), Expect = 26  
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
 LDD CCSR  
 Sbjct: 330 LDDQAFCCSR 339

>gi|14484312|gb|AAE63497.1| Sequence 1 from patent US 6207416  
gi|17905611|gb|AAE80914.1| Sequence 1 from patent US 6287759  
 Length = 1693

Score = 22.3 bits (45), Expect = 26  
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
 LDD CCSR  
 Sbjct: 330 LDDQAFCCSR 339

>gi|1613525|gb|AAB16505.1| Sequence 2 from patent US 5559095

gi|1830459|gb|AAB44913.1| Sequence 2 from patent US 5587454  
gi|4000574|gb|AAC94006.1|AR024748 Sequence 2 from patent US 5795864  
gi|5942569|gb|AAE02101.1| Sequence 2 from patent US 5859186  
gi|5972562|gb|AAE12453.1| Sequence 2 from patent US 5824645  
gi|7223963|gb|AAE24130.1| Sequence 2 from patent US 5891849  
gi|10054011|gb|AAE30918.1| Sequence 2 from patent US 5965534  
gi|10064284|gb|AAE38708.1| Sequence 2 from patent US 5994305  
gi|12815626|gb|AAE45435.1| Sequence 2 from patent US 6087091  
gi|14477864|gb|AAE61427.1| Sequence 2 from patent US 6136786  
 Length = 25

Score = 22.3 bits (45), Expect = 26  
 Identities = 8/13 (61%), Positives = 9/13 (69%), Gaps = 1/13 (7%)

Query: 14 DCCSRKCNRFNKC 26  
           DCC+  CNR  KC  
 Sbjct: 14 DCCTGSCNR-GKC 25

>gi|1613542|gb|AAB16522.1| Sequence 19 from patent US 5559095  
gi|1830476|gb|AAB44930.1| Sequence 19 from patent US 5587454  
gi|4000591|gb|AAC94023.1|AR024765 Sequence 19 from patent US 5795864  
gi|5942586|gb|AAE02118.1| Sequence 19 from patent US 5859186  
gi|5972579|gb|AAE12470.1| Sequence 19 from patent US 5824645  
gi|7223980|gb|AAE24147.1| Sequence 19 from patent US 5891849  
gi|10064318|gb|AAE38725.1| Sequence 19 from patent US 5994305  
gi|12815643|gb|AAE45452.1| Sequence 19 from patent US 6087091  
gi|14477881|gb|AAE61444.1| Sequence 19 from patent US 6136786  
 Length = 26

Score = 21.8 bits (44), Expect = 35  
 Identities = 8/13 (61%), Positives = 8/13 (61%)

Query: 14 DCCSRKCNRFNKC 26  
           DCCS  C R  KC  
 Sbjct: 14 DCCSGSCGRSGKC 26

>gi|1613531|gb|AAB16511.1| Sequence 8 from patent US 5559095  
gi|1830465|gb|AAB44919.1| Sequence 8 from patent US 5587454  
gi|4000580|gb|AAC94012.1|AR024754 Sequence 8 from patent US 5795864  
gi|5942575|gb|AAE02107.1| Sequence 8 from patent US 5859186  
gi|5972568|gb|AAE12459.1| Sequence 8 from patent US 5824645  
gi|7223969|gb|AAE24136.1| Sequence 8 from patent US 5891849  
gi|10064296|gb|AAE38714.1| Sequence 8 from patent US 5994305  
gi|12815632|gb|AAE45441.1| Sequence 8 from patent US 6087091  
gi|14477870|gb|AAE61433.1| Sequence 8 from patent US 6136786  
 Length = 26

Score = 21.8 bits (44), Expect = 35  
 Identities = 8/13 (61%), Positives = 8/13 (61%)

Query: 14 DCCSRKCNRFNKC 26  
           DCCS  C R  KC  
 Sbjct: 14 DCCSGSCGRSGKC 26

>gi|14092871|gb|AAE51612.1| Sequence 4 from patent US 6130039

gi|18093808|emb|CAD20397.1| unnamed protein product [Homo sapiens]  
Length = 727

Score = 21.8 bits (44), Expect = 35  
Identities = 7/13 (53%), Positives = 8/13 (61%), Gaps = 5/13 (38%)

Query: 1 CRIPNQKCFQHLD 13  
CRI FQ+LD  
Sbjct: 204 CRI-----FQNLD 211

>gi|4000083|gb|AAC93515.1|AR023217 Sequence 55 from patent US 5792846  
gi|59999999|gb|AAE21903.1| Sequence 55 from patent US 5851824  
Length = 1079

Score = 21.4 bits (43), Expect = 47  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
CFQHL  
Sbjct: 303 CFQHL 307

>gi|7224006|gb|AAE24173.1| Sequence 2 from patent US 5891857  
gi|14101230|gb|AAE53547.1| Sequence 2 from patent US 6149903  
gi|14112621|gb|AAE58038.1| Sequence 2 from patent US 6177410  
gi|20229343|gb|AAE90486.1| Sequence 49 from patent US 6342483  
Length = 1863

Score = 21.4 bits (43), Expect = 47  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
CFQHL  
Sbjct: 1225 CFQHL 1229

Score = 16.8 bits (32), Expect = 1184  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 24 NKCVC 27  
NKCVC  
Sbjct: 799 NKCVC 802

>gi|23342653|emb|CAD48690.1| unnamed protein product [Homo sapiens]  
gi|23342655|emb|CAD48691.1| unnamed protein product [Homo sapiens]  
gi|23342659|emb|CAD48693.1| unnamed protein product [Homo sapiens]  
Length = 457

Score = 21.4 bits (43), Expect = 47  
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 3 IPNQKCFQHL 12  
IP QKC HL  
Sbjct: 291 IPEQKCNPHL 300

>gi|5946864|gb|AAE03769.1| Sequence 20 from patent US 5866542  
gi|5947165|gb|AAE04070.1| Sequence 20 from patent US 5866543  
gi|5954014|gb|AAE06518.1| Sequence 20 from patent US 5872098  
gi|10050408|gb|AAE27315.1| Sequence 20 from patent US 5955294  
gi|12816345|gb|AAE46154.1| Sequence 20 from patent US 6087487  
 Length = 100

Score = 21.4 bits (43), Expect = 47  
 Identities = 8/15 (53%), Positives = 8/15 (53%), Gaps = 5/15 (33%)

Query: 12 LDDC-----CSRKCN 21  
           LDDC      C   KCN  
 Sbjct: 35 LDDCGTQKPCEAKCN 49

>gi|4000084|gb|AAC93516.1|AR023218 Sequence 56 from patent US 5792846  
gi|6000000|gb|AAE21904.1| Sequence 56 from patent US 5851824  
 Length = 1084

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8   CFQHL 12  
           CFQHL  
 Sbjct: 303 CFQHL 307

>gi|3209905|gb|AAC20849.1|I81608 Sequence 4 from patent US 5710019  
 Length = 494

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
           LDDCC  
 Sbjct: 123 LDDCC 127

>gi|14100343|gb|AAE53483.1| Sequence 4 from patent US 6140485  
 Length = 1091

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8   CFQHL 12  
           CFQHL  
 Sbjct: 303 CFQHL 307

>gi|5946896|gb|AAE03801.1| Sequence 62 from patent US 5866542  
gi|5947197|gb|AAE04102.1| Sequence 62 from patent US 5866543  
gi|5954046|gb|AAE06550.1| Sequence 62 from patent US 5872098  
gi|10050440|gb|AAE27347.1| Sequence 62 from patent US 5955294  
gi|12816377|gb|AAE46186.1| Sequence 62 from patent US 6087487  
 Length = 171

Score = 21.4 bits (43), Expect = 47  
 Identities = 7/13 (53%), Positives = 7/13 (53%), Gaps = 5/13 (38%)

Query: 14 DC-----CSRKCN 21  
           DC      C RKN  
 Sbjct: 101 DCGNDKQCERKCN 113

>gi|15141758|emb|CAC50182.1| Orf1 [Hepatitis E virus]  
           Length = 1708

Score = 21.4 bits (43), Expect = 47  
 Identities = 6/10 (60%), Positives = 7/10 (70%), Gaps = 3/10 (30%)

Query: 12 LDD---CCSR 18  
           LBD     CCSR  
 Sbjct: 330 LBDQAFCCSR 339

>gi|23342657|emb|CAD48692.1| unnamed protein product [Homo sapiens]  
           Length = 457

Score = 21.4 bits (43), Expect = 47  
 Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 3 IPNQKCFQHL 12  
          IP QKC HL  
 Sbjct: 291 IPEQKCNPHL 300

>gi|3014969|gb|AAC11849.1|I78815 Sequence 2 from patent US 5693473  
gi|3209867|gb|AAC20811.1|I81570 Sequence 2 from patent US 5709999  
gi|3209873|gb|AAC20817.1|I81576 Sequence 2 from patent US 5710001  
gi|3992676|gb|AAC86103.1|AR005620 Sequence 2 from patent US 5747282  
gi|3994270|gb|AAC87698.1|AR008672 Sequence 2 from patent US 5753441  
gi|14478556|gb|AAE61797.1| Sequence 2 from patent US 6162897  
           Length = 1863

Score = 21.4 bits (43), Expect = 47  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 8 CFQHL 12  
          CFQHL  
 Sbjct: 1225 CFQHL 1229

Score = 16.8 bits (32), Expect = 1184  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 24 NKCVC 27  
           NKCVC  
 Sbjct: 799 NKCVC 802

Get selected sequences

Select all  
Deselect all

Database: Protein sequences derived from the Patent division of  
GenBank

Posted date: Nov 25, 2002 1:06 AM  
Number of letters in database: 16,453,681  
Number of sequences in database: 104,350

Lambda	K	H
0.355	0.288	2.12

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Hits to DB: 912,208

Number of Sequences: 104350

Number of extensions: 21292

Number of successful extensions: 3537

Number of sequences better than 20000.0: 3253

Number of HSP's better than 20000.0 without gapping: 3253

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 3536

length of query: 27

length of database: 16,453,681

effective HSP length: 18

effective length of query: 9

effective length of database: 14,575,381

effective search space: 131178429

effective search space used: 131178429

T: 11

A: 40

X1: 14 ( 7.2 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 23 (13.6 bits)

S2: 23 (12.9 bits)



## NR Gen PVIIA Search

### BLASTP 2.2.4 [Aug-26-2002]

#### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038288080-013595-3111

#### Query=

(27 letters)

**Database:** All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

1,242,768 sequences; 395,571,179 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

#### Taxonomy reports

#### Distribution of 150 Blast Hits on the Query Sequence

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Sequences producing significant alignments:		Score (bits)	E Value
<a href="#">gi 3891872 pdb 1KCP </a>	3d Structure Of K-Conotoxin Pviia, A ...	45	8e-05
<a href="#">gi 7519866 pir  A58997</a>	kappa-conotoxin PVIIA - cone shell (...)	45	8e-05
<a href="#">gi 3891964 pdb 1AV3 </a>	Potassium Channel Blocker Kappa Conot...	45	8e-05
<a href="#">gi 22002036 sp P56633 CXK7 CONPU</a>	Kappa-conotoxin PVIIA prec...	45	8e-05
<a href="#">gi 21402496 ref NP_658481.1 </a>	minC, Bacterial proteins invol...	28	15
<a href="#">gi 12656031 gb AAK00711.1 AF228515.1</a>	polyprotein [Clitoria ...	24	275
<a href="#">gi 17533597 ref NP_495391.1 </a>	Putative membrane protein, wit...	23	369
<a href="#">gi 310662 gb AAA30048.1 </a>	ETS homologue	23	495
<a href="#">gi 15603466 ref NP_246540.1 </a>	TagI [Pasteurella multocida] >...	23	495
<a href="#">gi 99609 pir  S14947</a>	2S albumin - Brazil nut >gi 17713 emb ...	23	495
<a href="#">gi 18571020 ref XP_095628.1 </a>	hypothetical protein XP_095628...	23	495
<a href="#">gi 23047878 gb ZP_00075808.1 </a>	hypothetical protein [Methano...	22	664
<a href="#">gi 90454 pir  S01845</a>	DNA (cytosine-5-)-methyltransferase (E...	22	664
<a href="#">gi 13878219 ref NP_113566.1 </a>	ribonuclease/angiogenin inhibi...	22	664

<a href="#">gi 2689716 gb AAC40061.1 </a>	DNA (cytosine-5)-methyltransferas...	22	664
<a href="#">gi 7339827 gb AAF60965.1 </a>	DNA methyltransferase [Mus muscul...	22	664
<a href="#">gi 12002701 gb AAG43376.1 AF155874_1</a>	putative cytosine DNA ...	22	664
<a href="#">gi 1765919 emb CAA32910.1 </a>	DNA methyltransferase 1 [Mus mus...	22	664
<a href="#">gi 6753664 ref NP_034196.1 </a>	DNA methyltransferase (cytosine...	22	664
<a href="#">gi 24475410 dbj BAC22660.1 </a>	plexinB1 [Mus musculus]	22	890
<a href="#">gi 15596236 ref NP_249730.1 </a>	conserved hypothetical protein...	21	1195
<a href="#">gi 7434825 pir  T13810</a>	DNA-directed DNA polymerase (EC 2.7....	21	1195
<a href="#">gi 1272304 gb AAB01144.1 </a>	alpha esterase	21	1195
<a href="#">gi 6325231 ref NP_015299.1 </a>	multicopy suppressor of snf3 an...	21	1195
<a href="#">gi 24585481 ref NP_610051.2 </a>	CG9316-PA [Drosophila melanoga...	21	1195
<a href="#">gi 24583179 ref NP_609327.2 </a>	CG31712-PA [Drosophila melanog...	21	1195
<a href="#">gi 23468631 gb ZP_00123966.1 </a>	hypothetical protein [Pseudom...	21	1195
<a href="#">gi 19527983 gb AAL90106.1 </a>	AT19096p [Drosophila melanogaster]	21	1195
<a href="#">gi 25032745 ref XP_206420.1 </a>	hypothetical protein XP_206420...	21	1195
<a href="#">gi 7661970 ref NP_055455.1 </a>	KIAA0173 gene product [Homo sap...	21	1195
<a href="#">gi 20070166 ref NP_002227.2 </a>	potassium voltage-gated channe...	21	1195
<a href="#">gi 16945371 emb CAB97275.2 </a>	conserved hypothetical protein ...	21	1195
<a href="#">gi 7513252 pir  JC5919</a>	potassium channel 1 - human >gi 2739...	21	1195
<a href="#">gi 2494180 sp Q27607 DPG1 DROME</a>	DNA polymerase gamma subuni...	21	1195
<a href="#">gi 12849875 dbj BAB28515.1 </a>	Hbs1-like (S. cerevisiae)~data ...	21	1195
<a href="#">gi 12619543 gb AAG60433.1 AF215005_1</a>	conotoxin scaffold VI/...	21	1195
<a href="#">gi 19074436 ref NP_585942.1 </a>	similarity to GCN1-LIKE TRANSL...	21	1195
<a href="#">gi 23475177 gb ZP_00130466.1 </a>	hypothetical protein [Desulfo...	21	1195
<a href="#">gi 19527699 gb AAL89964.1 </a>	AT02241p [Drosophila melanogaster]	21	1195
<a href="#">gi 13358405 ref NP_078748.1 </a>	hypothetical protein [Lymphocy...	21	1195
<a href="#">gi 16944565 emb CAC18184.2 </a>	conserved hypothetical protein ...	21	1195
<a href="#">gi 21288647 gb EAA00940.1 </a>	agCP12708 [Anopheles gambiae str...	21	1195
<a href="#">gi 11359505 pir  T50956</a>	hypothetical protein B24P7.110 [imp...	21	1195
<a href="#">gi 25146207 ref NP_741523.1 </a>	Glycosyl transferase (38.8 kD)...	21	1195
<a href="#">gi 24644854 ref NP_524267.2 </a>	CG1257-PA [Drosophila melanoga...	21	1195
<a href="#">gi 7505021 pir  T34006</a>	hypothetical protein H43I07.2 - Caen...	21	1195
<a href="#">gi 6478764 gb AAF13991.1 AF200581_3</a>	coat protein [Soybean m...	21	1195
<a href="#">gi 22055778 ref XP_090213.5 </a>	hypothetical protein XP_090213...	21	1195
<a href="#">gi 21293200 gb EAA05345.1 </a>	agCP9199 [Anopheles gambiae str....	21	1195
<a href="#">gi 21553101 ref NP_660128.1 </a>	afamin precursor; alpha albumi...	21	1195
<a href="#">gi 15233602 ref NP_194676.1 </a>	putative protein; protein id: ...	21	1195
<a href="#">gi 17136648 ref NP_476821.1 </a>	CG8987-PA [Drosophila melanoga...	21	1195
<a href="#">gi 11890594 gb AAG41136.1 </a>	polyprotein [Soybean mosaic viru...	21	1195
<a href="#">gi 6478701 gb AAF13964.1 AF200554_2</a>	coat protein [Soybean m...	21	1195
<a href="#">gi 22964283 gb ZP_00011889.1 </a>	hypothetical protein [Rhodops...	21	1195
<a href="#">gi 20072386 gb AAH26681.1 </a>	Unknown (protein for IMAGE:50644...	21	1195
<a href="#">gi 17158399 ref NP_477819.1 </a>	wsv297 [shrimp white spot synd...	21	1195
<a href="#">gi 20845975 ref XP_137981.1 </a>	similar to potassium voltage-g...	21	1195
<a href="#">gi 15616394 ref NP_244699.1 </a>	BH3832~unknown [Bacillus halod...	21	1195
<a href="#">gi 20090341 ref NP_616416.1 </a>	potassium uptake protein [Meth...	21	1195
<a href="#">gi 21295843 gb EAA07988.1 </a>	agCP1575 [Anopheles gambiae str....	21	1195
<a href="#">gi 1435084 emb CAA67549.1 </a>	zinc finger protein [Ascobolus i...	21	1195
<a href="#">gi 1438541 gb AAB04099.1 </a>	sarcoendoplasmic reticulum Ca2+ A...	21	1603
<a href="#">gi 1815634 gb AAC44800.1 </a>	glutamine synthetase type 1	21	1603
<a href="#">gi 21672065 gb AAM74427.1 AC123594_10</a>	Putative lipid transf...	21	1603
<a href="#">gi 19920032 gb AAM08471.1 </a>	hypothetical protein [Dictyostel...	21	1603
<a href="#">gi 15224439 ref NP_181342.1 </a>	hypothetical protein; protein ...	21	1603
<a href="#">gi 6760665 gb AAD45537.2 AF164678_1</a>	FLASH homolog RIP25 [Ho...	21	1603
<a href="#">gi 13376109 ref NP_079042.1 </a>	hypothetical protein FLJ23451 ...	21	1603
<a href="#">gi 17545702 ref NP_519104.1 </a>	HYPOTHETICAL PROTEIN [Ralstoni...	21	1603
<a href="#">gi 18584880 ref XP_102118.1 </a>	hypothetical protein XP_102118...	21	1603
<a href="#">gi 1905981 gb AAB50229.1 </a>	Gal/GalNAc lectin heavy subunit [...	21	1603
<a href="#">gi 6681641 dbj BAA88816.1 </a>	Yb-B19L [Yaba monkey tumor virus]	21	1603
<a href="#">gi 21233883 ref NP_640181.1 </a>	hypothetical protein [Proteus ...	21	1603
<a href="#">gi 18676383 emb CAD21521.1 </a>	Brachyury [Podocoryne carnea]	21	1603

<a href="#">gi 20521882 dbj BAA92553.2 </a>	KIAA1315 protein [Homo sapiens]	<a href="#">21</a>	1603
<a href="#">gi 11288744 pir  T49852</a>	hypothetical protein B24P11.80 [imp...	<a href="#">21</a>	1603
<a href="#">gi 16197658 emb CAC82967.1 </a>	putative transposition protein ...	<a href="#">21</a>	1603
<a href="#">gi 13508551 emb CAC35152.1 </a>	TniB protein [Achromobacter xyl...	<a href="#">21</a>	1603
<a href="#">gi 20810180 gb AAH29359.1 </a>	similar to hypothetical protein ...	<a href="#">21</a>	1603
<a href="#">gi 18397365 ref NP_566259.1 </a>	Lon protease, putative; protei...	<a href="#">21</a>	1603
<a href="#">gi 23601348 ref XP_178510.1 </a>	hypothetical protein XP_178510...	<a href="#">21</a>	1603
<a href="#">gi 20091070 ref NP_617145.1 </a>	predicted protein [Methanosarc...	<a href="#">21</a>	1603
<a href="#">gi 15920020 ref NP_361080.1 </a>	TniB protein [Plasmid pSB102] ...	<a href="#">21</a>	1603
<a href="#">gi 23509421 ref NP_702088.1 </a>	hypothetical protein [Plasmodi...	<a href="#">21</a>	1603
<a href="#">gi 15805858 ref NP_294556.1 </a>	conserved hypothetical protein...	<a href="#">21</a>	1603
<a href="#">gi 7949131 ref NP_058025.1 </a>	ATPase, Ca++ transporting, ubiq...	<a href="#">21</a>	1603
<a href="#">gi 21299840 gb EAA11985.1 </a>	agCP8898 [Anopheles gambiae str...	<a href="#">21</a>	1603
<a href="#">gi 17548954 ref NP_522294.1 </a>	HYPOTHETICAL PROTEIN [Ralstoni...	<a href="#">21</a>	1603
<a href="#">gi 6912288 ref NP_036247.1 </a>	CASP8 associated protein 2; FLI...	<a href="#">21</a>	1603
<a href="#">gi 21291427 gb EAA03572.1 </a>	agCP14274 [Anopheles gambiae str...	<a href="#">21</a>	1603
<a href="#">gi 20346229 ref XP_109250.1 </a>	ATPase, Ca++ transporting, ubi...	<a href="#">21</a>	1603
<a href="#">gi 7662376 ref NP_055698.1 </a>	KIAA0914 gene product [Homo sap...	<a href="#">21</a>	1603
<a href="#">gi 121226 sp P13578 GLB3 TYLHE</a>	Globin IIB, extracellular (E...	<a href="#">21</a>	1603
<a href="#">gi 6753288 ref NP_036127.1 </a>	caspase 8 associated protein 2;...	<a href="#">21</a>	1603
<a href="#">gi 23509386 ref NP_702053.1 </a>	hypothetical protein [Plasmodi...	<a href="#">21</a>	1603
<a href="#">gi 7439466 pir  S71915</a>	hemoglobin, extracellular, chain B -...	<a href="#">21</a>	1603
<a href="#">gi 12057020 emb CAC19873.1 </a>	putative notch receptor protein...	<a href="#">21</a>	1603
<a href="#">gi 1389559 gb AAB02882.1 </a>	glycoprotein 330	<a href="#">21</a>	1603
<a href="#">gi 21672069 gb AAM74431.1 AC123594_14</a>	Putative lipid tranfe...	<a href="#">21</a>	1603

## Alignments

Get selected sequences

Select all

Deselect all

>[gi|3891872|pdb|1KCP|](#) 3d Structure Of K-Conotoxin Pviia, A Novel Potassium  
Channel-Blocking Toxin From Cone Snails, Nmr, 22  
Structures  
Length = 28

Score = 45.2 bits (99), Expect = 8e-05

Identities = 19/27 (70%), Positives = 19/27 (70%)

Query: 1 CXIXNQXCXQHLDDCCSXXCNXXNXCXV 27  
C I NQ C QHLDDCCS CN N CV  
Sbjct: 1 CRIXNQKCFQHLDDCCSRKCNRFNKCXV 27

>[gi|7519866|pir||A58997](#) kappa-conotoxin PVIIA - cone shell (Conus purpurascens)  
Length = 27

Score = 45.2 bits (99), Expect = 8e-05

Identities = 18/27 (66%), Positives = 18/27 (66%)

Query: 1 CXIXNQXCXQHLDDCCSXXCNXXNXCXV 27  
C I NQ C QHLDDCCS CN N CV  
Sbjct: 1 CRIPNQKCFQHLDDCCSRKCNRFNKCXV 27

>gi|3891964|pdb|1AV3| Potassium Channel Blocker Kappa Conotoxin Pviia From C.  
Purpurascens, Nmr, 20 Structures  
Length = 27

Score = 45.2 bits (99), Expect = 8e-05  
Identities = 19/27 (70%), Positives = 19/27 (70%)

Query: 1 CXIXNQXCXQHLDDCCSXXCNXXNXCXV 27  
C I NQ C QHLDDCCS CN N CV  
Sbjct: 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27

>gi|22002036|sp|P56633|CXK7 CONPU Kappa-conotoxin PVIIA precursor (Fin-popping peptide)  
Length = 72

Score = 45.2 bits (99), Expect = 8e-05  
Identities = 18/27 (66%), Positives = 18/27 (66%)

Query: 1 CXIXNQXCXQHLDDCCSXXCNXXNXCXV 27  
C I NQ C QHLDDCCS CN N CV  
Sbjct: 46 CRIPNQKCFQHLDDCCSRKCNRFNKCV 72

>gi|21402496|ref|NP\_658481.1| minC, Bacterial proteins involved in chromosomal  
partitioning  
[Bacillus anthracis A2012]  
Length = 228

Score = 27.8 bits (58), Expect = 15  
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 11 HLDDCCS 17  
HLDDCCS  
Sbjct: 21 HLDDCCS 27

>gi|12656031|gb|AAK00711.1|AF228515\_1 polyprotein [Clitoria virus Y]  
Length = 489

Score = 23.5 bits (48), Expect = 275  
Identities = 6/9 (66%), Positives = 7/9 (77%)

Query: 8 CXQHLDDCC 16  
C QH+D CC  
Sbjct: 197 CAQHIDGCC 205

>gi|17533597|ref|NP\_495391.1| Putative membrane protein, with at least 2 transmembrane  
domains  
[Caenorhabditis elegans]  
gi|7500246|pir||T16223 hypothetical protein F31E8.4 - Caenorhabditis elegans  
gi|1280155|gb|AAA98020.1| Hypothetical protein F31E8.4 [Caenorhabditis elegans]  
Length = 162

Score = 23.1 bits (47), Expect = 369  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 10 QHLDDCC 16  
 QHL DCC  
 Sbjct: 156 QHLTDCC 162

>gi|310662|gb|AAA30048.1| ETS homologue  
 Length = 559

Score = 22.7 bits (46), Expect = 495  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 11 HLDDCC 16  
 HLD+CC  
 Sbjct: 22 HLDECC 27

>gi|15603466|ref|NP\_246540.1| TagI [Pasteurella multocida]  
gi|12721997|gb|AAK03685.1| TagI [Pasteurella multocida]  
 Length = 183

Score = 22.7 bits (46), Expect = 495  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 11 HLDDCC 16  
 HL+DCC  
 Sbjct: 176 HLNDCC 181

>gi|99609|pir||S14947 2S albumin - Brazil nut  
gi|17713|emb|CAA38363.1| 2S albumin [Bertholletia excelsa]  
 Length = 154

Score = 22.7 bits (46), Expect = 495  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 11 HLDDCC 16  
 HLD+CC  
 Sbjct: 86 HLDECC 91

>gi|18571020|ref|XP\_095628.1| hypothetical protein XP\_095628 [Homo sapiens]  
 Length = 276

Score = 22.7 bits (46), Expect = 495  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 11 HLDDCCS 17  
 HL DCCS  
 Sbjct: 99 HLKDCCS 105

>gi|23047878|gb|ZP\_00075808.1| hypothetical protein [Methanosarcina barkeri]  
 Length = 175

Score = 22.3 bits (45), Expect = 664  
 Identities = 5/7 (71%), Positives = 7/7 (100%)

Query: 10 QHLDDCC 16  
 Q+LD+CC  
 Sbjct: 155 QNLDECC 161

>gi|90454|pir||S01845 DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - mouse  
 Length = 1573

Score = 22.3 bits (45), Expect = 664  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
 C QHLDD  
 Sbjct: 242 CGQHLDD 248

>gi|13878219|ref|NP\_113566.1| ribonuclease/angiogenin inhibitor 2 [Mus musculus]  
gi|13603845|gb|AAK31960.1|AF285581.1 ribonuclease/angiogenin inhibitor 2 [Mus musculus]  
 Length = 748

Score = 22.3 bits (45), Expect = 664  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 1/11 (9%)

Query: 3 IXNQXCXQHLD 13  
 I NQ C QHLD  
 Sbjct: 453 IQNQ-CLQHLD 462

>gi|2689716|gb|AAC40061.1| DNA (cytosine-5)-methyltransferase [Mus musculus]  
 Length = 1502

Score = 22.3 bits (45), Expect = 664  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
 C QHLDD  
 Sbjct: 243 CGQHLDD 249

>gi|7339827|gb|AAF60965.1| DNA methyltransferase [Mus musculus]  
gi|9719249|gb|AAF97695.1| DNA (cytosine-5)-methyltransferase [Mus musculus]  
 Length = 1502

Score = 22.3 bits (45), Expect = 664  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
 C QHLDD  
 Sbjct: 244 CGQHLDD 250

>gi|12002701|gb|AAG43376.1|AF155874.1 putative cytosine DNA methyltransferase [Oryza sativa]  
 Length = 1501

Score = 22.3 bits (45), Expect = 664  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
C QHLDD  
Sbjct: 243 CGQHLDD 249

>gi|1765919|emb|CAA32910.1| DNA methyltransferase 1 [Mus musculus]  
Length = 1620

Score = 22.3 bits (45), Expect = 664  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
C QHLDD  
Sbjct: 361 CGQHLDD 367

>gi|6753664|ref|NP\_034196.1| DNA methyltransferase (cytosine-5) [Mus musculus]  
gi|20141336|sp|P13864|DNM1 MOUSE DNA (cytosine-5)-methyltransferase 1 (Dnmt1) (DNA  
methyltransferase  
MmuI) (DNA MTase MmuI) (MCMT) (M.MmuI) (Met-1)  
gi|6625687|gb|AAF19352.1| DNA methyltransferase [Mus musculus]  
Length = 1620

Score = 22.3 bits (45), Expect = 664  
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
C QHLDD  
Sbjct: 362 CGQHLDD 368

>gi|24475410|dbj|BAC22660.1| plexinB1 [Mus musculus]  
Length = 2119

Score = 21.8 bits (44), Expect = 890  
Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 1/10 (10%)

Query: 8 CXQHLD-DCC 16  
C QHLD D C  
Sbjct: 482 CAQHLD DCDSC 491

>gi|15596236|ref|NP\_249730.1| conserved hypothetical protein [Pseudomonas aeruginosa  
PA01]  
gi|11347735|pir||G83515 conserved hypothetical protein PA1039 [imported] - Pseudomonas  
aeruginosa (strain PA01)  
gi|9946952|gb|AAG04428.1|AE004536 7 conserved hypothetical protein [Pseudomonas  
aeruginosa PA01]  
Length = 157

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 14 LDDCC 18

>gi|7434825|pir||T13810 DNA-directed DNA polymerase (EC 2.7.7.7) gamma, mitochondrial -  
 fruit fly (*Drosophila melanogaster*)  
gi|2289912|gb|AAC47658.1| mitochondrial DNA polymerase catalytic subunit precursor  
 [*Drosophila melanogaster*]  
 Length = 1145

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 662 LDDCC 666

>gi|1272304|gb|AAB01144.1| alpha esterase  
 Length = 548

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDDC 15  
 +HLDDC  
 Sbjct: 273 EHLDDC 278

>gi|6325231|ref|NP\_015299.1| multicopy suppressor of snf3 and grr1 mutants; Skslp  
 [*Saccharomyces cerevisiae*]  
gi|2499625|sp|Q12505|SKS1 YEAST Serine/threonine-protein kinase SKS1 (Suppressor  
 kinase of SNF3)  
gi|2133138|pir||S61935 SKS1 protein - yeast (*Saccharomyces cerevisiae*)  
gi|1039451|gb|AAB68161.1| Sha3p  
gi|1173541|gb|AAC49570.1| Skslp  
 Length = 502

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/7 (71%), Positives = 7/7 (100%)

Query: 11 HLDDCCS 17  
 H+D+CCS  
 Sbjct: 243 HVDECCS 249

>gi|24585481|ref|NP\_610051.2| CG9316-PA [*Drosophila melanogaster*]  
gi|22946930|gb|AAF53915.2| CG9316-PA [*Drosophila melanogaster*]  
 Length = 448

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC



Sbjct: 236 LDDCC 240

>gi|24583179|ref|NP\_609327.2| CG31712-PA [Drosophila melanogaster]  
gi|22946070|gb|AAF52833.2| CG31712-PA [Drosophila melanogaster]  
 Length = 309

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 216 LDDCC 220

>gi|23468631|gb|ZP\_00123966.1| hypothetical protein [Pseudomonas syringae pv. syringae B728a]  
 Length = 610

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 304 LDDCC 308

>gi|19527983|gb|AAL90106.1| AT19096p [Drosophila melanogaster]  
 Length = 447

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 234 LDDCC 238

>gi|25032745|ref|XP\_206420.1| hypothetical protein XP\_206420 [Mus musculus]  
 Length = 118

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15  
 HLDDC  
 Sbjct: 10 HHLDDC 15

>gi|7661970|ref|NP\_055455.1| KIAA0173 gene product [Homo sapiens]  
gi|20455377|sp|Q14679|Y173 HUMAN Hypothetical protein KIAA0173  
gi|1136406|dbj|BAA11490.1| similar to pig tubulin-tyrosine ligase. [Homo sapiens]  
 Length = 1199

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 12 LDDCCS 17  
 L+DCCS  
 Sbjct: 519 LEDCCS 524

>gi|20070166|ref|NP\_002227.2| potassium voltage-gated channel, subfamily F, member 1;  
 potassium  
     channel KH1 [Homo sapiens]  
gi|24418476|sp|Q9H3M0|KCF1 HUMAN Potassium voltage-gated channel subfamily F member 1  
 (Voltage-gated  
     potassium channel protein Kv5.1) (KH1)  
gi|12001824|gb|AAG43055.1| potassium channel [Homo sapiens]  
gi|19913491|gb|AAH26110.1| potassium voltage-gated channel, subfamily F, member 1  
 [Homo  
     sapiens]  
 Length = 494

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 123 LDDCC 127

>gi|16945371|emb|CAB97275.2| conserved hypothetical protein [Neurospora crassa]  
 Length = 1405

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDDC 15  
 +HLDDC  
 Sbjct: 1182 EHLDDC 1187

>gi|7513252|pir||JC5919 potassium channel.1 - human  
gi|2739501|gb|AAC05597.1| potassium channel [Homo sapiens]  
 Length = 494

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 123 LDDCC 127

>gi|2494180|sp|Q27607|DPG1\_DROME DNA polymerase gamma subunit 1, mitochondrial  
 precursor  
     (Mitochondrial DNA polymerase catalytic subunit)  
gi|7447799|pir||T13808 DNA-directed DNA polymerase (EC 2.7.7.7) gamma chain - fruit  
 fly  
     (Drosophila melanogaster)  
gi|1401344|gb|AAC47290.1| DNA polymerase gamma  
 Length = 1145

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
           LDDCC  
 Sbjct: 662 LDDCC 666

>gi|12849875|dbj|BAB28515.1| Hbs1-like (S. cerevisiae)~data source:MGD, source  
 key:MGI:1891704,  
       evidence:ISS~putative [Mus musculus]  
       Length = 211

Score = 21.4 bits (43), Expect = 1195  
 Identities = 7/13 (53%), Positives = 7/13 (53%), Gaps = 6/13 (46%)

Query: 11 HLD-----DCCS 17  
           HLD          DCCS  
 Sbjct: 163 HLDSSSKPFDCCS 175

>gi|12619543|gb|AAG60433.1|AF215005.1 conotoxin scaffold VI/VII precursor [Conus  
 ventricosus]  
       Length = 74

Score = 21.4 bits (43), Expect = 1195  
 Identities = 7/10 (70%), Positives = 7/10 (70%), Gaps = 1/10 (10%)

Query: 8 CXQHLDCCS 17  
          C QH DCCS  
 Sbjct: 55 CTQH-SDCCS 63

>gi|19074436|ref|NP\_585942.1| similarity to GCN1-LIKE TRANSLATIONAL ACTIVATOR  
 [Encephalitozoon  
   cuniculi]  
gi|19069078|emb|CAD25546.1| similarity to GCN1-LIKE TRANSLATIONAL ACTIVATOR  
 [Encephalitozoon  
   cuniculi]  
       Length = 1323

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 12 LDDCCS 17  
           LD+CCS  
 Sbjct: 779 LDECCS 784

>gi|23475177|gb|ZP\_00130466.1| hypothetical protein [Desulfovibrio desulfuricans G20]  
       Length = 589

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 10 QHLDDCC 16  
           Q LD+CC

Sbjct: 203 QRLDECC 209

>gi|19527699|gb|AA189964.1| AT02241p [Drosophila melanogaster]  
Length = 1145

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LDDCC

Sbjct: 662 LDDCC 666

>gi|13358405|ref|NP\_078748.1| hypothetical protein [Lymphocystis disease virus 1]  
Length = 1085

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LDDCC

Sbjct: 825 LDDCC 829

>gi|16944565|emb|CAC18184.2| conserved hypothetical protein [Neurospora crassa]  
Length = 590

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDDC 15  
+HLDDC

Sbjct: 374 EHLDDC 379

>gi|21288647|gb|EAA00940.1| agCP12708 [Anopheles gambiae str. PEST]  
Length = 552

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LDDCC

Sbjct: 207 LDDCC 211

>gi|11359505|pir||T50956 hypothetical protein B24P7.110 [imported] - Neurospora crassa  
Length = 979

Score = 21.4 bits (43), Expect = 1195  
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDDC 15  
+HLDDC

Sbjct: 756 EHLDDC 761

>gi|25146207|ref|NP\_741523.1| Glycosyl transferase (38.8 kD) [Caenorhabditis elegans]  
gi|17402836|gb|AAL38962.1|AF125965\_3 Hypothetical protein H43I07.3 [Caenorhabditis elegans]

Length = 339

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 100 LDDCC 104

>gi|24644854|ref|NP\_524267.2| CG1257-PA [Drosophila melanogaster]  
gi|17862822|gb|AAL39888.1| LP07235p [Drosophila melanogaster]  
gi|23170575|gb|AAF54004.2| CG1257-PA [Drosophila melanogaster]  
gi|25012462|gb|AAN71336.1| RE24420p [Drosophila melanogaster]

Length = 543

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 10 QHLDDC 15  
 +HLDDC  
 Sbjct: 273 EHLDDC 278

>gi|7505021|pir||T34006 hypothetical protein H43I07.2 - Caenorhabditis elegans  
 Length = 697

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 100 LDDCC 104

>gi|6478764|gb|AAF13991.1|AF200581\_3 coat protein [Soybean mosaic virus]  
 Length = 277

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 11 HLDDCC 16  
 H+DDCC  
 Sbjct: 1 HVDDCC 6

>gi|22055778|ref|XP\_090213.5| hypothetical protein XP\_090213 [Homo sapiens]  
 Length = 705

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 249 LDDCC 253

>gi|21293200|gb|EAA05345.1| agCP9199 [Anopheles gambiae str. PEST]  
 Length = 1129

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LDDCC  
 Sbjct: 331 LDDCC 335

>gi|21553101|ref|NP\_660128.1| afamin precursor; alpha albumin [Mus musculus]  
gi|5902744|sp|O89020|AFAM MOUSE Afamin precursor (Alpha-albumin) (Alpha-Alb)  
gi|3646361|emb|CAA09471.1| alpha-albumin protein [Mus musculus]  
 Length = 611

Score = 21.4 bits (43), Expect = 1195  
 Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 12 LDDCCS 17  
 L+DCCS  
 Sbjct: 381 LEDCCS 386

Get selected sequences  
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 Deselect all

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Nov 25, 2002 1:38 AM  
 Number of letters in database: 395,571,179  
 Number of sequences in database: 1,242,768

Lambda	K	H
0.357	0.284	2.14

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30  
 Gap Penalties: Existence: 9, Extension: 1  
 Number of Hits to DB: 8,008,999  
 Number of Sequences: 1242768  
 Number of extensions: 61346  
 Number of successful extensions: 1959  
 Number of sequences better than 20000.0: 1939  
 Number of HSP's better than 20000.0 without gapping: 1939

Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1959  
length of query: 27  
length of database: 395,571,179  
effective HSP length: 18  
effective length of query: 9  
effective length of database: 373,201,355  
effective search space: 3358812195  
effective search space used: 3358812195  
T: 11  
A: 40  
X1: 14 ( 7.2 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 34 (19.3 bits)  
S2: 34 (17.6 bits)

## Pat Gen PVIIA Search

### BLASTP 2.2.4 [Aug-26-2002]

#### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038288110-013776-17050

#### Query=

(27 letters)

**Database:** Protein sequences derived from the Patent division of GenBank

104,350 sequences; 16,453,681 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

#### Taxonomy reports

#### Distribution of 162 Blast Hits on the Query Sequence

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Sequences producing significant alignments:		Score (bits)	E Value
<a href="#">gi 3209905 gb AAC20849.1 I81608</a>	Sequence 4 from patent US 5...	<u>21</u>	47
<a href="#">gi 14118421 gb AAE59660.1 </a>	Sequence 90 from patent US 6187548	<u>21</u>	63
<a href="#">gi 14118419 gb AAE59658.1 </a>	Sequence 86 from patent US 6187548	<u>21</u>	63
<a href="#">gi 14118420 gb AAE59659.1 </a>	Sequence 88 from patent US 6187548	<u>21</u>	63
<a href="#">gi 15124758 gb AAE73219.1 </a>	Sequence 84 from patent US 6239270	<u>21</u>	63
<a href="#">gi 14118418 gb AAE59657.1 </a>	Sequence 84 from patent US 6187548	<u>21</u>	63
<a href="#">gi 5950802 gb AAE05028.1 </a>	Sequence 2 from patent US 5869282...	<u>21</u>	84
<a href="#">gi 3209904 gb AAC20848.1 I81607</a>	Sequence 2 from patent US 5...	<u>21</u>	84
<a href="#">gi 21438796 emb CAD34785.1 </a>	unnamed protein product [Homo s...	<u>20</u>	113
<a href="#">gi 3997978 gb AAC91410.1 AR017520</a>	Sequence 2 from patent US...	<u>20</u>	113
<a href="#">gi 18674819 emb CAD23295.1 </a>	unnamed protein product [Homo s...	<u>20</u>	151
<a href="#">gi 12824450 gb AAE49356.1 </a>	Sequence 1 from patent US 6110686	<u>20</u>	151
<a href="#">gi 15121659 gb AAE72339.1 </a>	Sequence 9 from patent US 623570...	<u>20</u>	151
<a href="#">gi 21508815 gb AAM58270.1 </a>	Sequence 1 from patent US 6379925	<u>20</u>	151
<a href="#">gi 1831307 gb AAB45761.1 </a>	Sequence 13 from patent US 5591821	<u>19</u>	203



<a href="#">gi 1254372 gb AAA95626.1 </a>	Sequence 6 from patent US 5482928...	19	203
<a href="#">gi 1831303 gb AAB45757.1 </a>	Sequence 4 from patent US 5591821	19	203
<a href="#">gi 512010 emb CAA01442.1 </a>	ovine IL-1 beta [Ovis sp.]	19	203
<a href="#">gi 1613525 gb AAB16505.1 </a>	Sequence 2 from patent US 5559095...	19	203
<a href="#">gi 21065816 emb CAD32046.1 </a>	unnamed protein product [synthe...	19	272
<a href="#">gi 14110683 gb AAE57223.1 </a>	Sequence 6 from patent US 617181...	19	272
<a href="#">gi 4526603 emb CAA00457.1 </a>	MAB MBrl VK sequence [synthetic ...	19	272
<a href="#">gi 14103731 gb AAE55165.1 </a>	Sequence 8 from patent US 6153740	19	272
<a href="#">gi 14103728 gb AAE55162.1 </a>	Sequence 4 from patent US 6153740	19	272
<a href="#">gi 14110681 gb AAE57221.1 </a>	Sequence 2 from patent US 617181...	19	272
<a href="#">gi 14110684 gb AAE57224.1 </a>	Sequence 7 from patent US 6171816	19	272
<a href="#">gi 12813715 gb AAE45015.1 </a>	Sequence 20 from patent US 6083904	19	272
<a href="#">gi 14103730 gb AAE55164.1 </a>	Sequence 6 from patent US 6153740	19	272
<a href="#">gi 14103729 gb AAE55163.1 </a>	Sequence 5 from patent US 6153740	19	272
<a href="#">gi 270588 gb AAA02097.1 </a>	Sequence 2 from Patent US 4879374	19	272
<a href="#">gi 3994136 gb AAC87564.1 AR007930</a>	Sequence 17 from patent U...	19	272
<a href="#">gi 14110685 gb AAE57225.1 </a>	Sequence 8 from patent US 6171816	19	272
<a href="#">gi 1830486 gb AAB44940.1 </a>	Sequence 29 from patent US 558745...	18	365
<a href="#">gi 14119703 gb AAE60017.1 </a>	Sequence 8 from patent US 619087...	18	365
<a href="#">gi 3011710 gb AAC11158.1 I75569</a>	Sequence 3 from patent US 5...	18	365
<a href="#">gi 1613542 gb AAB16522.1 </a>	Sequence 19 from patent US 555909...	18	365
<a href="#">gi 1831302 gb AAB45756.1 </a>	Sequence 3 from patent US 5591821	18	365
<a href="#">gi 2725130 gb AAB92812.1 I67150</a>	Sequence 21 from patent US ...	18	365
<a href="#">gi 4774193 emb CAB42495.1 </a>	unnamed protein product [unident...	18	365
<a href="#">gi 413431 emb CAA00767.1 </a>	ORF2 [synthetic construct]	18	365
<a href="#">gi 10049538 gb AAE26445.1 </a>	Sequence 13 from patent US 5948900	18	365
<a href="#">gi 12807911 gb AAE43131.1 </a>	Sequence 4 from patent US 6074840	18	365
<a href="#">gi 3011709 gb AAC11157.1 I75568</a>	Sequence 2 from patent US 5...	18	365
<a href="#">gi 21065678 emb CAD32037.1 </a>	unnamed protein product [Homo s...	18	365
<a href="#">gi 20241673 gb AAE92344.1 </a>	Sequence 338 from patent US 6348328	18	365
<a href="#">gi 3994135 gb AAC87563.1 AR007929</a>	Sequence 16 from patent U...	18	365
<a href="#">gi 18674249 emb CAD23272.1 </a>	unnamed protein product [Homo s...	18	365
<a href="#">gi 3994138 gb AAC87566.1 AR007932</a>	Sequence 19 from patent U...	18	365
<a href="#">gi 3011708 gb AAC11156.1 I75567</a>	Sequence 1 from patent US 5...	18	365
<a href="#">gi 14097464 gb AAE52306.1 </a>	Sequence 5 from patent US 6133232	18	365
<a href="#">gi 20241956 gb AAE92627.1 </a>	Sequence 6 from patent US 6348348	18	365
<a href="#">gi 12711156 emb CAC28493.1 </a>	At position 11, R is a purine. ...	18	365
<a href="#">gi 1613531 gb AAB16511.1 </a>	Sequence 8 from patent US 5559095...	18	365
<a href="#">gi 6740790 emb CAB69452.1 </a>	ANTI FREEZE PROTEIN [Daucus carota]	18	365
<a href="#">gi 1830478 gb AAB44932.1 </a>	Sequence 21 from patent US 558745...	18	365
<a href="#">gi 1831725 gb AAB46179.1 </a>	Sequence 2 from patent US 5597707...	18	365
<a href="#">gi 1831305 gb AAB45759.1 </a>	Sequence 9 from patent US 5591821	18	365
<a href="#">gi 17915749 gb AAE84475.1 </a>	Sequence 10 from patent US 63070...	18	365
<a href="#">gi 3995759 gb AAC89187.1 AR013309</a>	Sequence 3 from patent US...	18	365
<a href="#">gi 17915747 gb AAE84473.1 </a>	Sequence 8 from patent US 630701...	18	365
<a href="#">gi 5946864 gb AAE03769.1 </a>	Sequence 20 from patent US 586654...	18	490
<a href="#">gi 19701037 emb CAD29042.1 </a>	unnamed protein product [Homo s...	18	490
<a href="#">gi 5946861 gb AAE03766.1 </a>	Sequence 7 from patent US 5866542...	18	490
<a href="#">gi 5946859 gb AAE03764.1 </a>	Sequence 4 from patent US 5866542...	18	490
<a href="#">gi 16223597 gb AAE74949.1 </a>	Sequence 2 from patent US 6251655	18	658
<a href="#">gi 2489762 gb AAB77898.1 I59399</a>	Sequence 4 from patent US 5...	18	658
<a href="#">gi 10053997 gb AAE30904.1 </a>	Sequence 3 from patent US 596552...	18	658
<a href="#">gi 594162 gb AAA55769.1 </a>	Sequence 17 from Patent EP 0324648	18	658
<a href="#">gi 10049907 gb AAE26814.1 </a>	Sequence 12 from patent US 59522...	18	658
<a href="#">gi 14106039 gb AAE55654.1 </a>	Sequence 23 from patent US 6160088	18	658
<a href="#">gi 4001198 gb AAC94630.1 AR025722</a>	Sequence 2 from patent US...	18	658
<a href="#">gi 21336360 emb CAD33448.1 </a>	unnamed protein product [Homo s...	18	658
<a href="#">gi 23316741 gb AAN21265.1 </a>	Sequence 2 from patent US 6416734	18	658
<a href="#">gi 16223478 gb AAE74874.1 </a>	Sequence 2 from patent US 6251636	18	658
<a href="#">gi 10053996 gb AAE30903.1 </a>	Sequence 2 from patent US 596552...	18	658
<a href="#">gi 2484109 gb AAB72245.1 I49138</a>	Sequence 8 from patent US 5...	18	658

<u>gi 21538090 emb CAD35982.1 </u>	prepro-PAPP-A2 coding sequence ...	<u>18</u>	658
<u>gi 12829122 gb AAE50822.1 </u>	Sequence 2 from patent US 6127159	<u>18</u>	658
<u>gi 9997807 emb CAC07548.1 </u>	unnamed protein product [Mus mus...	<u>18</u>	658
<u>gi 23329052 gb AAN25969.1 </u>	Sequence 22 from patent US 6428967	<u>18</u>	658
<u>gi 21438806 emb CAD34790.1 </u>	unnamed protein product [Homo s...	<u>18</u>	658
<u>gi 20241852 gb AAE92523.1 </u>	Sequence 517 from patent US 6348328	<u>18</u>	658
<u>gi 3211666 gb AAC21426.1 I83369</u>	Sequence 16 from patent US ...	<u>18</u>	658
<u>gi 10188331 emb CAC09134.1 </u>	unnamed protein product [Zea mays]	<u>18</u>	658
<u>gi 3999143 gb AAC92575.1 AR021637</u>	Sequence 3 from patent US...	<u>18</u>	658
<u>gi 10054000 gb AAE30907.1 </u>	Sequence 6 from patent US 596552...	<u>18</u>	658
<u>gi 23329055 gb AAN25972.1 </u>	Sequence 25 from patent US 6428967	<u>18</u>	658
<u>gi 23329053 gb AAN25970.1 </u>	Sequence 23 from patent US 6428967	<u>18</u>	658
<u>gi 3208749 gb AAC20330.1 I80459</u>	Sequence 4 from patent US 5...	<u>18</u>	658
<u>gi 10057863 gb AAE34769.1 </u>	Sequence 6 from patent US 5977442	<u>18</u>	658
<u>gi 15797474 emb CAC88318.1 </u>	unnamed protein product [Homo s...	<u>18</u>	658
<u>gi 23329054 gb AAN25971.1 </u>	Sequence 24 from patent US 6428967	<u>18</u>	658
<u>gi 6733930 emb CAB69362.1 </u>	unnamed protein product [unident...	<u>18</u>	658
<u>gi 23329051 gb AAN25968.1 </u>	Sequence 21 from patent US 6428967	<u>18</u>	658
<u>gi 3999808 gb AAC93240.1 AR022942</u>	Sequence 9 from patent US...	<u>18</u>	658
<u>gi 10049906 gb AAE26813.1 </u>	Sequence 10 from patent US 59522...	<u>18</u>	658
<u>gi 12811284 gb AAE44297.1 </u>	Sequence 5 from patent US 608054...	<u>18</u>	658
<u>gi 5953850 gb AAE06354.1 </u>	Sequence 5 from patent US 5871964...	<u>18</u>	658
<u>gi 1606923 gb AAB09880.1 </u>	Sequence 4 from patent US 5491075...	<u>17</u>	883
<u>gi 3717241 emb CAA03733.1 </u>	unnamed protein product [Senna o...	<u>17</u>	883

## Alignments

Get selected sequences

Select all

Deselect all

>gi|3209905|gb|AAC20849.1|I81608 Sequence 4 from patent US 5710019  
Length = 494

Score = 21.4 bits (43), Expect = 47  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 12 LDDCC 16

LDDCC

Sbjct: 123 LDDCC 127

>gi|14118421|gb|AAE59660.1| Sequence 90 from patent US 6187548  
Length = 4655

Score = 21.0 bits (42), Expect = 63  
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDDC 15

HLDDC

Sbjct: 3096 HLDDC 3100

>gi|14118419|gb|AAE59658.1| Sequence 86 from patent US 6187548  
Length = 4655

Score = 21.0 bits (42), Expect = 63  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDDC 15  
 HLDDC  
 Sbjct: 3096 HLDDC 3100

>gi|14118420|gb|AAE59659.1| Sequence 88 from patent US 6187548  
 Length = 4655

Score = 21.0 bits (42), Expect = 63  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDDC 15  
 HLDDC  
 Sbjct: 3096 HLDDC 3100

>gi|15124758|gb|AAE73219.1| Sequence 84 from patent US 6239270  
 Length = 4654

Score = 21.0 bits (42), Expect = 63  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDDC 15  
 HLDDC  
 Sbjct: 3096 HLDDC 3100

>gi|14118418|gb|AAE59657.1| Sequence 84 from patent US 6187548  
 Length = 4655

Score = 21.0 bits (42), Expect = 63  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 11 HLDDC 15  
 HLDDC  
 Sbjct: 3096 HLDDC 3100

>gi|5950802|gb|AAE05028.1| Sequence 2 from patent US 5869282  
gi|10070027|gb|AAE41587.1| Sequence 2 from patent US 6004924  
 Length = 1404

Score = 20.6 bits (41), Expect = 84  
 Identities = 5/8 (62%), Positives = 7/8 (87%)

Query: 8 CXQHLDDC 15  
 C ++LDDC  
 Sbjct: 604 CAENLDDC 611

>gi|3209904|gb|AAC20848.1|I81607 Sequence 2 from patent US 5710019  
 Length = 513

Score = 20.6 bits (41), Expect = 84  
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16  
           HLD CC  
 Sbjct: 160 HLDGCC 165

>gi|21438796|emb|CAD34785.1| unnamed protein product [Homo sapiens]  
           Length = 1105

Score = 20.2 bits (40), Expect = 113  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 10 QHLDD 14  
           QHLDD  
 Sbjct: 749 QHLDD 753

>gi|3997978|gb|AAC91410.1|AR017520 Sequence 2 from patent US 5777094  
           Length = 1865

Score = 20.2 bits (40), Expect = 113  
 Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 10 QHLDD 14  
           QHLDD  
 Sbjct: 1510 QHLDD 1514

>gi|18674819|emb|CAD23295.1| unnamed protein product [Homo sapiens]  
           Length = 816

Score = 19.7 bits (39), Expect = 151  
 Identities = 5/7 (71%), Positives = 6/7 (85%)

Query: 8 CXQHLDD 14  
           C QHLD+  
 Sbjct: 110 CPQHLDE 116

>gi|12824450|gb|AAE49356.1| Sequence 1 from patent US 6110686  
           Length = 178

Score = 19.7 bits (39), Expect = 151  
 Identities = 6/8 (75%), Positives = 6/8 (75%), Gaps = 2/8 (25%)

Query: 10 QHL--DDC 15  
           QHL DDC  
 Sbjct: 125 QHLRLDDC 132

>gi|15121659|gb|AAE72339.1| Sequence 9 from patent US 6235708  
gi|16219471|gb|AAE74125.1| Sequence 9 from patent US 6245529  
           Length = 145

Score = 19.7 bits (39), Expect = 151

Identities = 6/8 (75%), Positives = 6/8 (75%), Gaps = 2/8 (25%)

Query: 10 QHL--DDC 15  
           QHL DDC  
 Sbjct: 103 QHLRLDDC 110

>gi|21508815|gb|AAM58270.1| Sequence 1 from patent US 6379925  
           Length = 1964

Score = 19.7 bits (39), Expect = 151  
 Identities = 5/8 (62%), Positives = 7/8 (87%)

Query: 8 CXQHLLDDC 15  
           C ++LDDC  
 Sbjct: 349 CEENLDDC 356

Score = 18.5 bits (36), Expect = 365  
 Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 8 CXQHLLDDC 15  
           C Q LD+C  
 Sbjct: 426 CHQDLDEC 433

>gi|1831307|gb|AAB45761.1| Sequence 13 from patent US 5591821  
           Length = 29

Score = 19.3 bits (38), Expect = 203  
 Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 14 DCCSXXCN 21  
           +CCS CN  
 Sbjct: 17 NCCSGSCN 24

>gi|1254372|gb|AAA95626.1| Sequence 6 from patent US 5482928  
gi|3012065|gb|AAC11513.1|I75924 Sequence 6 from patent US 5689048  
           Length = 25

Score = 19.3 bits (38), Expect = 203  
 Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 14 DCCSXXCN 21  
           DCC+ CN  
 Sbjct: 14 DCCTGSCN 21

>gi|1831303|gb|AAB45757.1| Sequence 4 from patent US 5591821  
           Length = 25

Score = 19.3 bits (38), Expect = 203  
 Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 14 DCCSXXCN 21

+CCS CN  
Sbjct: 14 NCCSGSCN 21

>gi|512010|emb|CAA01442.1| ovine IL-1 beta [Ovis sp.]  
Length = 266

Score = 19.3 bits (38), Expect = 203  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 8 CXQHLD 13  
C QHLD  
Sbjct: 34 CTQHLD 39

>gi|1613525|gb|AAB16505.1| Sequence 2 from patent US 5559095  
gi|1830459|gb|AAB44913.1| Sequence 2 from patent US 5587454  
gi|4000574|gb|AAC94006.1|AR024748 Sequence 2 from patent US 5795864  
gi|5942569|gb|AAE02101.1| Sequence 2 from patent US 5859186  
gi|5972562|gb|AAE12453.1| Sequence 2 from patent US 5824645  
gi|7223963|gb|AAE24130.1| Sequence 2 from patent US 5891849  
gi|10054011|gb|AAE30918.1| Sequence 2 from patent US 5965534  
gi|10064284|gb|AAE38708.1| Sequence 2 from patent US 5994305  
gi|12815626|gb|AAE45435.1| Sequence 2 from patent US 6087091  
gi|14477864|gb|AAE61427.1| Sequence 2 from patent US 6136786  
Length = 25

Score = 19.3 bits (38), Expect = 203  
Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 14 DCCSXXCN 21  
DCC+ CN  
Sbjct: 14 DCCTGSCN 21

>gi|21065816|emb|CAD32046.1| unnamed protein product [synthetic construct]  
Length = 2444

Score = 18.9 bits (37), Expect = 272  
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 12 LDDCCSXXCN 21  
LDDC S C+  
Sbjct: 642 LDDCASSPCD 651

Score = 16.8 bits (32), Expect = 1184  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 10 QHLD 13  
QHLD  
Sbjct: 1847 QHLD 1850

Score = 12.9 bits (23), Expect = 16694  
Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 16 CSXXCN 21  
 CS CN  
 Sbjct: 1464 CSLQCN 1469

>gi|14110683|gb|AAE57223.1| Sequence 6 from patent US 6171816  
gi|15592507|emb|CAC69704.1| unnamed protein product [Homo sapiens]  
 Length = 166

Score = 18.9 bits (37), Expect = 272  
 Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15  
 HL+DC  
 Sbjct: 66 HHLEDC 71

>gi|4526603|emb|CAA00457.1| MAb MBrl VK sequence [synthetic construct]  
 Length = 119

Score = 18.9 bits (37), Expect = 272  
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 8 CXQHLD 13  
 C QHLD  
 Sbjct: 98 CQQHLD 103

>gi|14103731|gb|AAE55165.1| Sequence 8 from patent US 6153740  
 Length = 648

Score = 18.9 bits (37), Expect = 272  
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LD+CC  
 Sbjct: 635 LDNCC 639

>gi|14103728|gb|AAE55162.1| Sequence 4 from patent US 6153740  
 Length = 650

Score = 18.9 bits (37), Expect = 272  
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
 LD+CC  
 Sbjct: 636 LDNCC 640

>gi|14110681|gb|AAE57221.1| Sequence 2 from patent US 6171816  
gi|15592501|emb|CAC69703.1| unnamed protein product [Homo sapiens]  
gi|17920557|gb|AAE86177.1| Sequence 106 from patent US 6312922  
 Length = 175

Score = 18.9 bits (37), Expect = 272  
 Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15  
       HLD+C  
 Sbjct: 76 HHLDEC 81

>gi|14110684|gb|AAE57224.1| Sequence 7 from patent US 6171816  
       Length = 183

Score = 18.9 bits (37), Expect = 272  
 Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15  
       HL+DC  
 Sbjct: 83 HHLEDC 88

>gi|12813715|gb|AAE45015.1| Sequence 20 from patent US 6083904  
       Length = 2556

Score = 18.9 bits (37), Expect = 272  
 Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 12 LDDCCSXXCN 21  
       LDDC S C+  
 Sbjct: 642 LDDCASSPCD 651

Score = 16.8 bits (32), Expect = 1184  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 10 QHLD 13  
       QHLD  
 Sbjct: 1847 QHLD 1850

Score = 12.9 bits (23), Expect = 16694  
 Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 16 CSXXCN 21  
       CS CN  
 Sbjct: 1464 CSLQCN 1469

>gi|14103730|gb|AAE55164.1| Sequence 6 from patent US 6153740  
       Length = 649

Score = 18.9 bits (37), Expect = 272  
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
       LD+CC  
 Sbjct: 635 LDNCC 639



>gi|14103729|gb|AAE55163.1| Sequence 5 from patent US 6153740  
Length = 649

Score = 18.9 bits (37), Expect = 272  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 12 LDDCC 16  
LD+CC  
Sbjct: 635 LDNCC 639

>gi|270588|gb|AAA02097.1| Sequence 2 from Patent US 4879374  
Length = 266

Score = 18.9 bits (37), Expect = 272  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 8 CXQHLD 13  
C QHLD  
Sbjct: 34 CIQHLD 39

>gi|3994136|gb|AAC87564.1|AR007930 Sequence 17 from patent US 5750652  
Length = 2556

Score = 18.9 bits (37), Expect = 272  
Identities = 6/10 (60%), Positives = 7/10 (70%)

Query: 12 LDDCCSXXCN 21  
LDDC S C+  
Sbjct: 642 LDDCASSPCD 651

Score = 16.8 bits (32), Expect = 1184  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 10 QHLD 13  
QHLD  
Sbjct: 1847 QHLD 1850

Score = 12.9 bits (23), Expect = 16694  
Identities = 4/6 (66%), Positives = 4/6 (66%)

Query: 16 CSXXCN 21  
CS CN  
Sbjct: 1464 CSLQCN 1469

>gi|14110685|gb|AAE57225.1| Sequence 8 from patent US 6171816  
Length = 170

Score = 18.9 bits (37), Expect = 272  
Identities = 4/6 (66%), Positives = 5/6 (83%)

Query: 10 QHLDDC 15  
 HL+DC  
 Sbjct: 70 HHLEDC 75

>gi|1830486|gb|AAB44940.1| Sequence 29 from patent US 5587454  
gi|4000601|gb|AAC94033.1|AR024775 Sequence 29 from patent US 5795864  
gi|5942596|gb|AAE02128.1| Sequence 29 from patent US 5859186  
gi|5972589|gb|AAE12480.1| Sequence 29 from patent US 5824645  
gi|7223990|gb|AAE24157.1| Sequence 29 from patent US 5891849  
gi|10064338|gb|AAE38735.1| Sequence 29 from patent US 5994305  
gi|12815653|gb|AAE45462.1| Sequence 29 from patent US 6087091  
gi|14477891|gb|AAE61454.1| Sequence 29 from patent US 6136786  
 Length = 26

Score = 18.5 bits (36), Expect = 365  
 Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20  
 DCCS C  
 Sbjct: 14 DCCSGSC 20

>gi|14119703|gb|AAE60017.1| Sequence 8 from patent US 6190876  
gi|20220418|gb|AAE86866.1| Sequence 8 from patent US 6319704  
gi|21517011|gb|AAM60425.1| Sequence 8 from patent US 6399350  
 Length = 749

Score = 18.5 bits (36), Expect = 365  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 13 DDCC 16  
 DDCC  
 Sbjct: 482 DDCC 485

>gi|3011710|gb|AAC11158.1|I75569 Sequence 3 from patent US 5688764  
 Length = 39

Score = 18.5 bits (36), Expect = 365  
 Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20  
 DCCS C  
 Sbjct: 13 DCCSGSC 19

>gi|1613542|gb|AAB16522.1| Sequence 19 from patent US 5559095  
gi|1830476|gb|AAB44930.1| Sequence 19 from patent US 5587454  
gi|4000591|gb|AAC94023.1|AR024765 Sequence 19 from patent US 5795864  
gi|5942586|gb|AAE02118.1| Sequence 19 from patent US 5859186  
gi|5972579|gb|AAE12470.1| Sequence 19 from patent US 5824645  
gi|7223980|gb|AAE24147.1| Sequence 19 from patent US 5891849  
gi|10064318|gb|AAE38725.1| Sequence 19 from patent US 5994305  
gi|12815643|gb|AAE45452.1| Sequence 19 from patent US 6087091  
gi|14477881|gb|AAE61444.1| Sequence 19 from patent US 6136786  
 Length = 26

Score = 18.5 bits (36), Expect = 365  
 Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20  
           DCCS C  
 Sbjct: 14 DCCSGSC 20

>gi|1831302|gb|AAB45756.1| Sequence 3 from patent US 5591821  
                           Length = 26

Score = 18.5 bits (36), Expect = 365  
 Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20  
           DCCS C  
 Sbjct: 14 DCCSGSC 20

>gi|2725130|gb|AAB92812.1|I67150 Sequence 21 from patent US 5670319  
gi|3208874|gb|AAC20455.1|I80584 Sequence 21 from patent US 5708142  
gi|3991852|gb|AAC85279.1|AR002803 Sequence 21 from patent US 5741667  
gi|5951378|gb|AAE05604.1| Sequence 21 from patent US 5869612  
                           Length = 28

Score = 18.5 bits (36), Expect = 365  
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 11 HLDDC 15  
           HLD+C  
 Sbjct: 24 HLDEC 28

>gi|4774193|emb|CAB42495.1| unnamed protein product [unidentified]  
                           Length = 2321

Score = 18.5 bits (36), Expect = 365  
 Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16  
           HLDD C  
 Sbjct: 350 HLDDAC 355

>gi|413431|emb|CAA00767.1| ORF2 [synthetic construct]  
                           Length = 167

Score = 18.5 bits (36), Expect = 365  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 13 DDCC 16  
           DDCC  
 Sbjct: 36 DDCC 39

>gi|10049538|gb|AAE26445.1| Sequence 13 from patent US 5948900  
Length = 306

Score = 18.5 bits (36), Expect = 365  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 12 LDDCCS 17  
LDDC S  
Sbjct: 297 LDDCSS 302

>gi|12807911|gb|AAE43131.1| Sequence 4 from patent US 6074840  
Length = 1253

Score = 18.5 bits (36), Expect = 365  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 13 DDCC 16  
DDCC  
Sbjct: 1093 DDCC 1096

>gi|3011709|gb|AAC11157.1|I75568 Sequence 2 from patent US 5688764  
Length = 39

Score = 18.5 bits (36), Expect = 365  
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20  
DCCS C  
Sbjct: 13 DCCSGNC 19

>gi|21065678|emb|CAD32037.1| unnamed protein product [Homo sapiens]  
Length = 777

Score = 18.5 bits (36), Expect = 365  
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 13 DDCCS 17  
D+CCS  
Sbjct: 35 DECCS 39

>gi|20241673|gb|AAE92344.1| Sequence 338 from patent US 6348328  
Length = 243

Score = 18.5 bits (36), Expect = 365  
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 13 DDCC 16  
DDCC  
Sbjct: 240 DDCC 243

>gi|3994135|gb|AAC87563.1|AR007929 Sequence 16 from patent US 5750652

gi|12813714|gb|AAE45014.1| Sequence 19 from patent US 6083904  
Length = 2471

Score = 18.5 bits (36), Expect = 365  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16  
HLDD C  
Sbjct: 374 HLDDAC 379

Score = 18.5 bits (36), Expect = 365  
Identities = 6/13 (46%), Positives = 8/13 (61%)

Query: 8 CXQHLLDDCCSXXC 20  
C + LD+C S C  
Sbjct: 1146 CEEQLDECASNPC 1158

>gi|18674249|emb|CAD23272.1| unnamed protein product [Homo sapiens]  
gi|21522704|emb|CAD35406.1| unnamed protein product [Homo sapiens]  
Length = 2470

Score = 18.5 bits (36), Expect = 365  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16  
HLDD C  
Sbjct: 373 HLDDAC 378

Score = 18.5 bits (36), Expect = 365  
Identities = 6/13 (46%), Positives = 8/13 (61%)

Query: 8 CXQHLLDDCCSXXC 20  
C + LD+C S C  
Sbjct: 1145 CEEQLDECASNPC 1157

>gi|3994138|gb|AAC87566.1|AR007932 Sequence 19 from patent US 5750652  
Length = 2703

Score = 18.5 bits (36), Expect = 365  
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 11 HLDDCC 16  
HLDD C  
Sbjct: 408 HLDDAC 413

Score = 14.6 bits (27), Expect = 5150  
Identities = 3/4 (75%), Positives = 4/4 (100%)

Query: 12 LDDC 15  
LD+C  
Sbjct: 1416 LDEC 1419

Score = 12.9 bits (23), Expect = 16694  
 Identities = 4/9 (44%), Positives = 6/9 (66%)

Query: 13 DDCCSXXCN 21  
 ++C S CN  
 Sbjct: 679 NECHSNPCN 687

>gi|3011708|gb|AAC11156.1|I75567 Sequence 1 from patent US 5688764  
 Length = 39

Score = 18.5 bits (36), Expect = 365  
 Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 14 DCCSXXC 20  
 DCCS C  
 Sbjct: 13 DCCSGNC 19

>gi|14097464|gb|AAE52306.1| Sequence 5 from patent US 6133232  
 Length = 979

Score = 18.5 bits (36), Expect = 365  
 Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 11 HLDDC 15  
 HLD+C  
 Sbjct: 798 HLDNC 802

Get selected sequences  
 Select all  
 Deselect all

Database: Protein sequences derived from the Patent division of  
 GenBank

Posted date: Nov 25, 2002 1:06 AM  
 Number of letters in database: 16,453,681  
 Number of sequences in database: 104,350

Lambda	K	H
0.357	0.284	2.14

Gapped		
Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30  
 Gap Penalties: Existence: 9, Extension: 1  
 Number of Hits to DB: 379,047  
 Number of Sequences: 104350  
 Number of extensions: 3808

Number of successful extensions: 641  
Number of sequences better than 20000.0: 623  
Number of HSP's better than 20000.0 without gapping: 623  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 641  
length of query: 27  
length of database: 16,453,681  
effective HSP length: 18  
effective length of query: 9  
effective length of database: 14,575,381  
effective search space: 131178429  
effective search space used: 131178429  
T: 11  
A: 40  
X1: 14 ( 7.2 bits)  
X2: 35 (14.8 bits)  
X3: 58 (24.6 bits)  
S1: 23 (13.7 bits)  
S2: 23 (12.9 bits)

Search for :

CHIXNQHCWQHLDCCSHHCNHNHNCV

Chose to make the most divergent peptide (still within scope of generic) to test what would match.

## BLASTP 2.2.4 [Aug-26-2002]

### Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1038288569-017646-1278

### Query=

(27 letters)

**Database:** All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

1,242,768 sequences; 395,571,179 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

### Taxonomy reports

### Distribution of 157 Blast Hits on the Query Sequence

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Sequences producing significant alignments:		Score (bits)	E Value
<a href="#">gi 3891872 pdb 1KCP </a>	3d Structure Of K-Conotoxin Pviia, A ...	52	6e-07
<a href="#">gi 7519866 pir  A58997</a>	kappa-conotoxin PVIIA - cone shell (...)	52	6e-07
<a href="#">gi 3891964 pdb 1AV3 </a>	Potassium Channel Blocker Kappa Conot...	52	6e-07
<a href="#">gi 22002036 sp P56633 CXK7</a>	CONPU Kappa-conotoxin PVIIA prec...	52	6e-07
<a href="#">gi 6907097 dbj BAA90624.1 </a>	Similar to Arabidopsis thaliana ...	29	4.5
<a href="#">gi 21402496 ref NP_658481.1 </a>	minC, Bacterial proteins invol...	28	15
<a href="#">gi 13376410 ref NP_079212.1 </a>	hypothetical protein FLJ23024 ...	27	26
<a href="#">gi 1085397 pir  S46487</a>	taurine transporter - human >gi 5598...	27	35
<a href="#">gi 1352535 sp P31641 S6A6</a>	HUMAN Sodium- and chloride-depend...	27	35
<a href="#">gi 13560627 gb AAK30132.1 AF346763</a>	1 intestinal taurine tra...	27	35



gi 23482928 gb EAA18766.1	hypothetical protein [Plasmodium...	27	35
gi 4507045 ref NP_003034.1	solute carrier family 6 (neurot...	27	35
gi 1708864 sp P98157 LRP1 CHICK	Low-density lipoprotein rec...	27	35
gi 13623303 gb AAH06252.1 AAH06252	Unknown (protein for MGC...	27	35
gi 21105785 gb AAM34790.1 AF512560_2	HAC4 [Arabidopsis thal...	26	47
gi 6010654 gb AAF01207.1 AF180526_1	E-septin short form [Ra...	26	47
gi 18405622 ref NP_564706.1	CREB-binding protein, putative...	26	47
gi 14794966 gb AAK73519.1	HAC4 [Arabidopsis thaliana]	26	47
gi 13929200 ref NP_114025.1	E-septin [Rattus norvegicus] >...	26	47
gi 20093168 ref NP_619243.1	hypothetical protein (multi-do...	26	47
gi 6090881 gb AAF03376.1 AF170253_1	septin-like protein [Ra...	26	47
gi 6683817 gb AAF23374.1	MLL septin-like fusion protein MS...	26	47
gi 17560900 ref NP_506264.1	Predicted CDS, major sperm pro...	26	47
gi 8778322 gb AAF79331.1 AC002304_24	F14J16.27 [Arabidopsis...	26	47
gi 5729933 ref NP_006631.1	MLL septin-like fusion; MLL sep...	26	47
gi 24656402 ref NP_611502.2	CG10438-PA [Drosophila melanog...	26	47
gi 22066365 ref XP_113892.2	similar to MLL septin-like fus...	26	47
gi 14530107 emb CAC42222.1	OVARIAN/Breast septin delta [Ho...	26	47
gi 6056385 gb AAF02849.1 AC009894_20	Unknown protein [Arabi...	26	47
gi 10433911 dbj BAB14057.1	unnamed protein product [Homo s...	26	47
gi 8393784 ref NP_059076.1	septin 9; MLL septin-like fusio...	26	47
gi 14530105 emb CAC42221.1	OVARIAN/Breast septin gamma [Ho...	26	47
gi 7512587 pir  T12519	hypothetical protein DKFZp434F243.1 ...	26	47
gi 4589626 dbj BAA76835.1	KIAA0991 protein [Homo sapiens] ...	26	47
gi 18582088 ref XP_090617.1	similar to Adenylate cyclase, ...	26	47
gi 6090911 gb AAF03391.1 AF173899_1	septin-like protein SLP...	26	47
gi 20892533 ref XP_156144.1	hypothetical protein XP_156144...	26	47
gi 23058070 gb ZP_00083175.1	hypothetical protein [Pseudom...	26	63
gi 24459580 gb AAN34381.1	envelope glycoprotein [Human imm...	26	63
gi 20844494 ref XP_137952.1	similar to putative retrovirus...	26	63
gi 9629632 ref NP_044917.1	tegument protein/FGARAT [murid ...	26	63
gi 23272552 gb AAH35574.1	chromosome 6 open reading frame ...	26	63
gi 13449287 ref NP_085155.1	NG3 protein [Homo sapiens] >gi...	26	63
gi 16924037 gb AAL31649.1 AC079179_4	Putative o-methyltran...	25	85
gi 23472065 gb ZP_00127393.1	hypothetical protein [Pseudom...	25	85
gi 20908811 ref XP_138742.1	similar to endogenous retrovir...	25	85
gi 15598375 ref NP_251869.1	conserved hypothetical protein...	25	85
gi 23058698 gb ZP_00083733.1	hypothetical protein [Pseudom...	25	85
gi 20468866 ref XP_117141.1	hypothetical protein XP_117141...	25	85
gi 15983410 gb AAL11573.1 AF424579_1	AT4g16570/dl4310w [Ara...	25	114
gi 22094360 gb AAM91887.1	putative cytokinin oxidase [Oryz...	25	114
gi 202106 gb AAA40468.1	transition protein 2' (alt.)	25	114
gi 110055 pir  S14529	transition protein 2 - mouse >gi 5487...	25	114
gi 18414696 ref NP_567508.1	expressed protein; protein id:...	25	114
gi 21302270 gb EAA14415.1	agCP8608 [Anopheles gambiae str....	25	114
gi 24817521 emb CAD54147.2	Hypothetical protein ZK757.4 [C...	25	114
gi 202105 gb AAA40467.1	transition protein 2 (alt.) >gi 12...	25	114
gi 17557071 ref NP_499189.1	DHHC zinc binding domain conta...	25	114
gi 12083591 ref NP_038722.2	transition protein 2 [Mus musc...	25	114
gi 24646280 ref NP_650191.1	CG5196-PA [Drosophila melanoga...	25	114
gi 15836695 ref NP_297383.1	tRNA delta(2)-isopentenylpyrop...	25	114
gi 20151945 gb AAM11332.1	GH06759p [Drosophila melanogaster]	25	114
gi 16519539 ref NP_443737.1	low density lipoprotein-relate...	25	114
gi 23055343 gb ZP_00081453.1	hypothetical protein [Geobact...	25	114
gi 13937291 gb AAK50122.1 AC087797_7	putative phospholipase...	25	114
gi 930024 emb CAA30824.1	tenascin [Gallus gallus]	24	153
gi 135584 sp P10039 TENA CHICK	Tenascin precursor (TN) (Hex...	24	153
gi 15230656 ref NP_187904.1	putative CREB-binding protein;...	24	153
gi 212748 gb AAA49085.1	190 kd tenascin precursor	24	153
gi 18546360 ref XP_099257.1	hypothetical protein XP_099257...	24	153
gi 212747 gb AAA49084.1	200 kd tenascin precursor	24	153

<a href="#">gi 21105780 gb AAM34788.1 AF512558.2</a>	HAC5 [Arabidopsis thal...	24	153
<a href="#">gi 15341664 gb AAH06778.1</a>	Unknown (protein for IMAGE:35890...	24	205
<a href="#">gi 2507193 sp P27704 MK06</a>	RAT Mitogen-activated protein kin...	24	205
<a href="#">gi 13928856 ref NP_113810.1</a>	mitogen-activated protein kina...	24	205
<a href="#">gi 24583179 ref NP_609327.2</a>	CG31712-PA [Drosophila melanog...	24	205
<a href="#">gi 22049606 ref XP_070277.2</a>	similar to Otoconin 90 precurs...	24	205
<a href="#">gi 23592724 ref XP_128141.2</a>	otoconin 90 [Mus musculus]	24	205
<a href="#">gi 4506139 ref NP_002759.1</a>	procollagen (type III) N-endope...	24	205
<a href="#">gi 22996345 gb ZP_00040604.1</a>	hypothetical protein [Xylella...	24	205
<a href="#">gi 22993598 gb ZP_00038168.1</a>	hypothetical protein [Xylella...	24	205
<a href="#">gi 13509205 emb CAC35209.1</a>	GRAAL2 protein [Drosophila mela...	24	205
<a href="#">gi 6682303 emb CAB64653.1</a>	GRAAL protein [Drosophila melano...	24	205
<a href="#">gi 7488985 pir  T17462</a>	disease resistance E - tomato >gi 42...	24	205
<a href="#">gi 15292455 gb AAK93496.1</a>	SD02860p [Drosophila melanogaster]	24	205
<a href="#">gi 18593306 ref XP_104434.1</a>	hypothetical protein XP_104434...	24	205
<a href="#">gi 21430770 gb AAM51063.1</a>	SD13780p [Drosophila melanogaster]	24	205
<a href="#">gi 4092677 gb AAC99455.1</a>	otoconin-90 [Mus musculus]	24	205
<a href="#">gi 17464262 ref XP_069418.1</a>	hypothetical protein XP_069418...	24	205
<a href="#">gi 16416462 dbj BAB70658.1</a>	spondin [Ciona savignyi]	24	205
<a href="#">gi 4176764 gb AAD08924.1</a>	otoconin-95 precursor [Mus musculus]	24	205
<a href="#">gi 16762646 ref NP_458263.1</a>	alpha-amylase [Salmonella ente...	24	205
<a href="#">gi 23239621 gb AAH35492.1</a>	similar to mitogen-activated pro...	24	205
<a href="#">gi 18858913 ref NP_571936.1</a>	jagged1 [Danio rerio] >gi 2045...	24	205
<a href="#">gi 16766949 ref NP_462564.1</a>	alpha-amylase [Salmonella typh...	24	205
<a href="#">gi 4506091 ref NP_002739.1</a>	mitogen-activated protein kinas...	24	205
<a href="#">gi 6225792 sp Q02509 OC90</a>	HUMAN Otoconin 90 precursor (Oc90...	24	205
<a href="#">gi 559705 dbj BAA07557.1</a>	The ha1551 gene is novel. [Homo s...	24	205
<a href="#">gi 24661359 ref NP_648288.1</a>	CG4821-PA [Drosophila melanoga...	24	205
<a href="#">gi 59977 emb CAA78662.1</a>	tripartite fusion transcript PLA2L...	24	205

## Alignments

Get selected sequences

Select all

Deselect all

>[gi|3891872|pdb|1KCP|](#) 3d Structure Of K-Conotoxin Pviia, A Novel Potassium Channel-Blocking Toxin From Cone Snails, Nmr, 22 Structures  
Length = 28

Score = 52.4 bits (116), Expect = 6e-07  
Identities = 19/27 (70%), Positives = 21/27 (77%)

Query: 1 CHIXNQHCWQHLDCCSHHCNHNHCV 27  
C I NQ C+QHLDCCS CN +N CV  
Sbjct: 1 CRIXNQKCFQHLDCCSRKCNRFNKCVC 27

>[gi|7519866|pir||A58997](#) kappa-conotoxin PVIIA - cone shell (Conus purpurascens)  
Length = 27

Score = 52.4 bits (116), Expect = 6e-07  
Identities = 18/27 (66%), Positives = 20/27 (74%)

Query: 1 CHIXNQHCWQHLDCCSHHCNHNHCV 27  
C I NQ C+QHLDCCS CN +N CV

Sbjct: 1 CRIPNQKCFQHLDDCCSRKCNRFNKCV 27

>gi|3891964|pdb|1AV3| Potassium Channel Blocker Kappa Conotoxin Pviia From C.  
Purpurascens, Nmr, 20 Structures  
Length = 27

Score = 52.4 bits (116), Expect = 6e-07  
Identities = 19/27 (70%), Positives = 21/27 (77%)

Query: 1 CHIXNQHCWQHLDDCCSHHCNHWNHCV 27  
C I NQ C+QHLDDCCS CN +N CV

Sbjct: 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27

>gi|22002036|sp|P56633|CXK7 CONPU Kappa-conotoxin PVIIA precursor (Fin-popping peptide)  
Length = 72

Score = 52.4 bits (116), Expect = 6e-07  
Identities = 18/27 (66%), Positives = 20/27 (74%)

Query: 1 CHIXNQHCWQHLDDCCSHHCNHWNHCV 27  
C I NQ C+QHLDDCCS CN +N CV

Sbjct: 46 CRIPNQKCFQHLDDCCSRKCNRFNKCV 72

>gi|6907097|dbj|BAA90624.1| Similar to Arabidopsis thaliana DNA chromosome 4, ESSA I  
contig  
fragment No. 6; calcium channel protein alpha-1 chain  
isoform A - rat. (Z97341) [Oryza sativa (japonica  
cultivar-group)]  
Length = 589

Score = 29.5 bits (62), Expect = 4.5  
Identities = 8/15 (53%), Positives = 9/15 (60%), Gaps = 4/15 (26%)

Query: 17 SHH----CNHWNHCV 27  
SHH C+HW CV

Sbjct: 292 SHHMKDWCDDHWKQCV 306

>gi|21402496|ref|NP\_658481.1| minC, Bacterial proteins involved in chromosomal  
partitioning  
[Bacillus anthracis A2012]  
Length = 228

Score = 27.8 bits (58), Expect = 15  
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 11 HLDDCCS 17  
HLDDCCS

Sbjct: 21 HLDDCCS 27

>gi|13376410|ref|NP\_079212.1| hypothetical protein FLJ23024 [Homo sapiens]  
gi|10439583|dbj|BAB15524.1| unnamed protein product [Homo sapiens]

Length = 279

Score = 26.9 bits (56), Expect = 26

Identities = 11/30 (36%), Positives = 11/30 (36%), Gaps = 17/30 (56%)

Query: 5 NQHCWQHLDCCSHHCNH-----WNHC 26  
 NQHC HCN WNHC  
 Sbjct: 157 NQHC-----EHCNSCTSKDGRKWNHC 177

>gi|1085397|pir|S46487 taurine transporter - human  
gi|559853|gb|AAA50842.1| placental taurine transporter  
 Length = 620

Score = 26.5 bits (55), Expect = 35

Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 161 HCNHWNTPHC 171

>gi|1352535|sp|P31641|S6A6 HUMAN . Sodium- and chloride-dependent taurine transporter  
gi|7441660|pir||G01426 taurine transporter - human  
gi|799339|gb|AAC50443.1| taurine transporter  
 Length = 620

Score = 26.5 bits (55), Expect = 35

Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 161 HCNHWNTPHC 171

>gi|13560627|gb|AAK30132.1|AF346763.1 intestinal taurine transporter [Homo sapiens]  
 Length = 244

Score = 26.5 bits (55), Expect = 35

Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 81 HCNHWNTPHC 91

>gi|23482928|gb|EAA18766.1| hypothetical protein [Plasmodium yoelii yoelii]  
 Length = 456

Score = 26.5 bits (55), Expect = 35

Identities = 11/24 (45%), Positives = 11/24 (45%), Gaps = 12/24 (50%)

Query: 6 QHCWQHLDCCSHHC-N--HWNHC 26  
 QH WQH C N HW HC  
 Sbjct: 188 QH-WQH-----CQNFQHWQHC 202

>gi|4507045|ref|NP\_003034.1| solute carrier family 6 (neurotransmitter transporter, taurine),  
 member 6; Solute carrier family 6 (neurotransmitter transporter, taurine), [Homo sapiens]  
gi|346388|pir||S29839 taurine transport protein - human  
gi|36727|emb|CAA79481.1| taurine transporter [Homo sapiens]  
gi|266092|gb|AAB25509.1| taurine transporter, HTAU [human, thyroid cells, Peptide, 619 aa]  
 Length = 619

Score = 26.5 bits (55), Expect = 35  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 161 HCNHSWNTPHC 171

>gi|1708864|sp|P98157|LRP1\_CHICK Low-density lipoprotein receptor-related protein 1 precursor (LRP)  
 (Alpha-2-macroglobulin receptor) (A2MR)  
gi|1079416|pir||A53102 alpha-2-macroglobulin receptor precursor - chicken  
gi|438007|emb|CAA52870.1| alpha-2-macroglobulin receptor [Gallus gallus]  
 Length = 4543

Score = 26.5 bits (55), Expect = 35  
 Identities = 8/18 (44%), Positives = 10/18 (55%), Gaps = 4/18 (22%)

Query: 7 HCWQHLLDDC----CSHHC 20  
 HC + L +C C HHC  
 Sbjct: 109 HCREQLANCTALGCQHHC 126

>gi|13623303|gb|AAH06252.1|AAH06252 Unknown (protein for MGC:10619) [Homo sapiens]  
 Length = 200

Score = 26.5 bits (55), Expect = 35  
 Identities = 8/11 (72%), Positives = 8/11 (72%), Gaps = 3/11 (27%)

Query: 19 HCNH-WN--HC 26  
 HCNH WN HC  
 Sbjct: 161 HCNHSWNTPHC 171

>gi|21105785|gb|AAM34790.1|AF512560\_2 HAC4 [Arabidopsis thaliana]  
 Length = 385

Score = 26.1 bits (54), Expect = 47  
 Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHHC-----NHW--NHC 26  
 HL CC HC N W NHC  
 Sbjct: 90 HLQHCCCK-HCTTLMVSGNRWVCNHC 113

>gi|6010654|gb|AAF01207.1|AF180526\_1 E-septin short form [Rattus norvegicus]

Length = 334

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 118 HINNENCWQ 126

>gi|18405622|ref|NP\_564706.1| CREB-binding protein, putative; protein id: At1g55970.1,  
supported by

cDNA: gi\_14794965 [Arabidopsis thaliana]  
Length = 1456

Score = 26.1 bits (54), Expect = 47  
Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHHC-----NHW--NHC 26  
HL CC HC N W NHC  
Sbjct: 1161 HLQHCK-HCTTLMVSGNRWVCNHC 1184

>gi|14794966|gb|AAK73519.1| HAC4 [Arabidopsis thaliana]  
Length = 413

Score = 26.1 bits (54), Expect = 47  
Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHHC-----NHW--NHC 26  
HL CC HC N W NHC  
Sbjct: 118 HLQHCK-HCTTLMVSGNRWVCNHC 141

>gi|13929200|ref|NP\_114025.1| E-septin [Rattus norvegicus]  
gi|6010652|gb|AAF01206.1|AF180525.1 E-septin long form [Rattus norvegicus]  
Length = 405

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 189 HINNENCWQ 197

>gi|20093168|ref|NP\_619243.1| hypothetical protein (multi-domain) [Methanosarcina  
acetivorans

str. C2A]  
gi|19918512|gb|AAM07723.1| hypothetical protein (multi-domain) [Methanosarcina  
acetivorans  
str. C2A]  
Length = 489

Score = 26.1 bits (54), Expect = 47  
Identities = 8/14 (57%), Positives = 9/14 (64%)

Query: 14 DCCSHHCNHNHCV 27  
 DCC H C+H H V  
 Sbjct: 463 DCCCHECDHHKHV 476

>gi|6090881|gb|AAF03376.1|AF170253.1 septin-like protein [Rattus norvegicus]  
 Length = 564

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 349 HINNENCWQ 357

>gi|6683817|gb|AAF23374.1| MLL septin-like fusion protein MSF-A [Homo sapiens]  
 Length = 586

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 369 HINNENCWQ 377

>gi|17560900|ref|NP\_506264.1| Predicted CDS, major sperm protein family member family member

[Caenorhabditis elegans]

gi|7503252|pir||T22096 hypothetical protein F42E8.2 - Caenorhabditis elegans

gi|3877039|emb|CAB01429.1| Hypothetical protein F42E8.2 [Caenorhabditis elegans]

Length = 122

Score = 26.1 bits (54), Expect = 47  
 Identities = 8/12 (66%), Positives = 8/12 (66%), Gaps = 2/12 (16%)

Query: 13 DDCCSHHCNHNHWN 24  
 D CASH C WN  
 Sbjct: 96 DACCASHC--WN 105

>gi|8778322|gb|AAF79331.1|AC002304.24 F14J16.27 [Arabidopsis thaliana]  
 Length = 1550

Score = 26.1 bits (54), Expect = 47  
 Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHHC-----NHW--NHC 26  
 HL CC HC N W NHC  
 Sbjct: 1229 HLQHCCK-HCTTLMVSGNRWVCNHC 1252

>gi|5729933|ref|NP\_006631.1| MLL septin-like fusion; MLL septin-like fusion (NOTE: non-standard symbol and name); septin D1 [Homo sapiens]

gi|5106557|gb|AAD39749.1|AF123052.1 MLL septin-like fusion protein [Homo sapiens]  
gi|11055011|gb|AAG27919.1|AF142408.1 cell division control protein septin D1 [Homo sapiens]  
gi|14530109|emb|CAC42223.1| OVARIAN/Breast septin alpha [Homo sapiens]  
gi|18203688|gb|AAH21192.1|AAH21192 MLL septin-like fusion [Homo sapiens]  
Length = 568

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 351 HINNENCWQ 359

>gi|24656402|ref|NP\_611502.2| CG10438-PA [Drosophila melanogaster]  
gi|24656406|ref|NP\_725988.1| CG30144-PA [Drosophila melanogaster]  
gi|7302348|gb|AAF57437.1| CG10438-PA [Drosophila melanogaster]  
gi|21626895|gb|AAM68396.1| CG30144-PA [Drosophila melanogaster]  
Length = 108

Score = 26.1 bits (54), Expect = 47  
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 1/10 (10%)

Query: 15 CCSHHCNH-W 23  
CC+H CNH W  
Sbjct: 97 CCNHECNHTW 106

>gi|22066365|ref|XP\_113892.2| similar to MLL septin-like fusion; MLL septin-like fusion  
(NOTE:  
non-standard symbol and name); septin D1 [Homo sapiens]  
Length = 569

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 352 HINNENCWQ 360

>gi|14530107|emb|CAC42222.1| OVARIAN/Breast septin delta [Homo sapiens]  
Length = 335

Score = 26.1 bits (54), Expect = 47  
Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
HI N++CWQ  
Sbjct: 118 HINNENCWQ 126

>gi|6056385|gb|AAF02849.1|AC009894.20 Unknown protein [Arabidopsis thaliana]  
Length = 1209

Score = 26.1 bits (54), Expect = 47



Identities = 11/25 (44%), Positives = 11/25 (44%), Gaps = 10/25 (40%)

Query: 11 HLDDCCSHHC-----NHW--NHC 26  
 HL CC HC N W NHC  
 Sbjct: 1152 HLQHCK-HCTTLMVSGNRWVCNHC 1175

>gi|10433911|dbj|BAB14057.1| unnamed protein product [Homo sapiens]  
 Length = 196

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 118 HINNENCWQ 126

>gi|8393784|ref|NP\_059076.1| septin 9; MLL septin-like fusion; SL3-3 integration site 1  
 [Mus musculus]  
gi|20347564|ref|XP\_109283.1| MLL septin-like fusion [Mus musculus]  
gi|6165419|emb|CAB59833.1| septin-like protein Sint1 [Mus musculus]  
gi|17980682|gb|AAL50685.1| septin 9 [Mus musculus]  
 Length = 334

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 118 HINNENCWQ 126

>gi|14530105|emb|CAC42221.1| OVARIAN/Breast septin gamma [Homo sapiens]  
 Length = 579

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 362 HINNENCWQ 370

>gi|7512587|pir||T12519 hypothetical protein DKFZp434F243.1 - human (fragment)  
gi|5262571|emb|CAB45728.1| hypothetical protein [Homo sapiens]  
 Length = 234

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 17 HINNENCWQ 25

>gi|4589626|dbj|BAA76835.1| KIAA0991 protein [Homo sapiens]  
gi|6683815|gb|AAF23373.1| MLL septin-like fusion protein MSF-B [Homo sapiens]  
gi|14530111|emb|CAC42224.1| OVARIAN/Breast septin beta [Homo sapiens]  
 Length = 422

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 205 HINNENCWQ 213

>gi|18582088|ref|XP\_090617.1| similar to Adenylate cyclase, type VII (ATP  
 pyrophosphate-lyase)  
 (Adenylyl cyclase) [Homo sapiens]  
 Length = 180

Score = 26.1 bits (54), Expect = 47  
 Identities = 7/12 (58%), Positives = 7/12 (58%), Gaps = 2/12 (16%)

Query: 7 HCWQHLDCCSH 18  
 CWQ DCCS  
 Sbjct: 25 QCWQR--DCCSQ 34

Score = 18.0 bits (35), Expect = 12551  
 Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 5 NQHC 8  
 NQHC  
 Sbjct: 148 NQHC 151

>gi|6090911|gb|AAF03391.1|AF173899 1 septin-like protein SLP-b [Rattus norvegicus]  
 Length = 479

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/9 (66%), Positives = 8/9 (88%)

Query: 2 HIXNQHCWQ 10  
 HI N++CWQ  
 Sbjct: 264 HINNENCWQ 272

>gi|20892533|ref|XP\_156144.1| hypothetical protein XP\_156144 [Mus musculus]  
 Length = 213

Score = 26.1 bits (54), Expect = 47  
 Identities = 6/8 (75%), Positives = 7/8 (87%)

Query: 5 NQHCWQHL 12  
 NQ CW+HL  
 Sbjct: 40 NQRCWEHL 47

>gi|23058070|gb|ZP\_00083175.1| hypothetical protein [Pseudomonas fluorescens]  
Length = 176

Score = 25.7 bits (53), Expect = 63  
Identities = 8/15 (53%), Positives = 8/15 (53%), Gaps = 5/15 (33%)

Query: 6 QHCWQHLDCCSHHC 20  
Q CW CCSH C  
Sbjct: 164 QRCW-----CCSHCC 173

>gi|24459580|gb|AAN34381.1| envelope glycoprotein [Human immunodeficiency virus 1]  
Length = 211

Score = 25.7 bits (53), Expect = 63  
Identities = 7/11 (63%), Positives = 7/11 (63%), Gaps = 4/11 (36%)

Query: 19 HCN-----HWNH 25  
HCN HWNH  
Sbjct: 63 HCNISKGHWNH 73

>gi|20844494|ref|XP\_137952.1| similar to putative retrovirus-related gag protein [Mus musculus]  
Length = 212

Score = 25.7 bits (53), Expect = 63  
Identities = 7/11 (63%), Positives = 8/11 (72%), Gaps = 1/11 (9%)

Query: 2 HIXNQHCWQHL 12  
HI NQ CW+ L  
Sbjct: 31 HI-NQQCWERL 40

>gi|9629632|ref|NP\_044917.1| tegument protein/FGARAT [murid herpesvirus 4]  
gi|2318002|gb|AAB66460.1| tegument protein/FGARAT [murid herpesvirus 4]  
gi|6625640|gb|AAF19341.1|AF105037.73 75a [murid herpesvirus 4]  
Length = 1291

Score = 25.7 bits (53), Expect = 63  
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 9 WQHLDD 14  
WQHLDD  
Sbjct: 1261 WQHLDD 1266

>gi|23272552|gb|AAH35574.1| chromosome 6 open reading frame 8 [Homo sapiens]  
Length = 293

Score = 25.7 bits (53), Expect = 63  
Identities = 10/22 (45%), Positives = 12/22 (54%), Gaps = 10/22 (45%)

Query: 7 HCWQHLD--DC-----CSHHC 20  
HC H+D +C CSHHC

Sbjct: 140 HC--HVDVDECRTSITLCSHHC 159

>gi|13449287|ref|NP\_085155.1| NG3 protein [Homo sapiens]  
gi|1841553|gb|AAB47494.1|AAB47494 NG3 [Homo sapiens]  
 Length = 293

Score = 25.7 bits (53), Expect = 63  
 Identities = 10/22 (45%), Positives = 12/22 (54%), Gaps = 10/22 (45%)

Query: 7 HCWQHLD--DC-----CSHHC 20  
 HC H+D +C CSHHC

Sbjct: 140 HC--HVDVDECRTSITLCSHHC 159

>gi|16924037|gb|AAL31649.1|AC079179.4 Putative o-methyltransferase ZRP4 [Oryza sativa]  
gi|17047043|gb|AAL34948.1|AC079037.21 Putative to o-methyltransferase ZRP4 [Oryza  
 sativa]  
 Length = 366

Score = 25.2 bits (52), Expect = 85  
 Identities = 7/9 (77%), Positives = 7/9 (77%), Gaps = 1/9 (11%)

Query: 7 HCWQHLD 15  
 HCWQ DDC

Sbjct: 271 HCWQD-DDC 278

>gi|23472065|gb|ZP\_00127393.1| hypothetical protein [Pseudomonas syringae pv. syringae  
 B728a]  
 Length = 409

Score = 25.2 bits (52), Expect = 85  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 21 NHWNHCV 27  
 NHW HCV

Sbjct: 194 NHWYHCV 200

>gi|20908811|ref|XP\_138742.1| similar to endogenous retroviral family W, env(C7),  
 member 1  
 (syncytin); envelope protein; syncytin [Homo sapiens]  
 [Mus musculus]  
 Length = 712

Score = 25.2 bits (52), Expect = 85  
 Identities = 12/26 (46%), Positives = 12/26 (46%), Gaps = 8/26 (30%)

Query: 1 CHIXNQHCWQHLDCCSHHCNHWNHC 26  
 CH HC Q L D C HH HC

Sbjct: 34 CH---HHCLQPLLDSCHHH-----HC 51

>gi|15598375|ref|NP\_251869.1| conserved hypothetical protein [Pseudomonas aeruginosa  
 PA01]

gi|11347983|pir||E83247 conserved hypothetical protein PA3179 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
gi|9949297|gb|AAG06567.1|AE004742.3 conserved hypothetical protein [Pseudomonas aeruginosa PA01]  
 Length = 386

Score = 25.2 bits (52), Expect = 85  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 21 NHWNHCV 27  
 NHW HCV  
 Sbjct: 191 NHWYHCV 197

>gi|23058698|gb|ZP\_00083733.1| hypothetical protein [Pseudomonas fluorescens]  
 Length = 448

Score = 25.2 bits (52), Expect = 85  
 Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 21 NHWNHCV 27  
 NHW HCV  
 Sbjct: 237 NHWYHCV 243

>gi|20468866|ref|XP\_117141.1| hypothetical protein XP\_117141 [Homo sapiens]  
 Length = 169

Score = 25.2 bits (52), Expect = 85  
 Identities = 8/13 (61%), Positives = 10/13 (76%), Gaps = 1/13 (7%)

Query: 15 CC-SHHCNHNHNC 26  
 CC SHH +H +HC  
 Sbjct: 128 CCLSHHRHRSNC 140

>gi|15983410|gb|AAL11573.1|AF424579.1 AT4g16570/dl4310w [Arabidopsis thaliana]  
gi|23308405|gb|AAN18172.1| At4g16570/dl4310w [Arabidopsis thaliana]  
 Length = 457

Score = 24.8 bits (51), Expect = 114  
 Identities = 5/8 (62%), Positives = 6/8 (75%)

Query: 20 CNHWNHCV 27  
 C+HW CV  
 Sbjct: 82 CDHWKQCV 89

Get selected sequences  
 Select all  
 Deselect all

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Nov 25, 2002 1:38 AM  
 Number of letters in database: 395,571,179

Number of sequences in database: 1,242,768

Lambda	K	H
0.359	0.268	2.40

Gapped

Lambda	K	H
0.294	0.110	0.610

Matrix: PAM30

Gap Penalties: Existence: 9, Extension: 1

Number of Hits to DB: 17,703,379

Number of Sequences: 1242768

Number of extensions: 331126

Number of successful extensions: 8258

Number of sequences better than 20000.0: 8042

Number of HSP's better than 20000.0 without gapping: 8050

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 8242

length of query: 27

length of database: 395,571,179

effective HSP length: 18

effective length of query: 9

effective length of database: 373,201,355

effective search space: 3358812195

effective search space used: 3358812195

T: 11

A: 40

X1: 14 ( 7.3 bits)

X2: 35 (14.8 bits)

X3: 58 (24.6 bits)

S1: 34 (19.5 bits)

S2: 34 (17.6 bits)

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Total number of pages: 1

Remarks:

Order of re-scan issued on .....